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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 07:54:49 ; Search time 122 Seconds
(without alignments)
11326.013 Million cell updates/sec

Title: US-10-069-304-1

Perfect score: 1944
Sequence: 1 atgtcttcggcgctctcc.....atagtgcacctctctttaa 1944

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCITUS.COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192.8	9.9	1593	4	US-09-602-472A-1
2	192.4	9.9	3108	4	US-10-101-464A-886
3	182	9.4	2868	3	US-09-228-986-4
4	182	9.4	2868	4	US-10-101-464A-4
5	179.8	9.2	1488	4	US-09-579-182-4
6	178.4	9.2	3239	3	US-09-228-986-9
7	178.4	9.2	3239	4	US-10-101-464A-9
8	176.4	9.1	1559	4	US-09-602-472A-3
9	174.6	9.0	2432	3	US-09-228-986-7
10	174.6	9.0	2432	4	US-10-101-464A-7
11	173	8.9	1457	4	US-10-101-464A-159
12	168.2	8.7	2175	4	US-10-101-464A-461
13	166.4	8.6	2749	1	US-08-265-628-1
14	162.4	8.4	4104	3	US-08-881-706-1
15	162.4	8.4	4104	4	US-09-823-394-1
16	162.2	8.3	2315	4	US-10-101-464A-874
17	160.2	8.2	4356	4	US-10-101-464A-888
18	159	8.2	758	4	US-10-101-464A-414
19	153.2	7.9	3257	4	US-10-101-464A-455
20	153.2	7.9	3257	4	US-10-101-464A-456
21	153.2	7.9	3715	4	US-10-101-464A-887
22	150.4	7.7	536	4	US-10-101-464A-355
23	149.8	7.6	493	4	US-10-101-464A-243
24	147.4	7.6	551	4	US-10-101-464A-305
25	146.8	7.6	2884	4	US-10-101-464A-291
26	146.8	7.6	3600	4	US-10-101-464A-458
27	146.6	7.5	2571	1	US-07-717-331F-9

28	146.6	7.5	2693	4	US-10-101-464A-873	Sequence 873, App
29	146.6	7.5	2833	1	US-07-717-331F-1	Sequence 1, Appl1
30	144.2	7.4	3222	4	US-10-101-464A-839	Sequence 839, App
31	140.6	7.2	1554	2	US-08-587-680A-24	Sequence 24, Appl
32	139.8	7.2	2114	4	US-09-602-472A-5	Sequence 5, Appl1
33	139.8	7.2	2749	1	US-07-717-331F-4	Sequence 4, Appl1
34	138.2	7.1	2389	3	US-09-228-986-1	Sequence 1, Appl1
35	138.2	7.1	2389	4	US-10-101-464A-1	Sequence 1, Appl1
36	137.4	7.1	771	4	US-10-101-464A-192	Sequence 192, App
37	136.6	7.0	383	4	US-10-101-464A-393	Sequence 393, App
38	135.6	7.0	3237	4	US-10-101-464A-858	Sequence 858, App
39	132.4	6.8	741	4	US-10-101-464A-385	Sequence 385, App
40	132	6.8	3361	4	US-10-101-464A-947	Sequence 947, App
41	131.8	6.8	2728	4	US-10-101-464A-862	Sequence 862, App
42	130.8	6.7	2336	3	US-09-228-986-10	Sequence 10, Appl
43	130.6	6.7	2336	4	US-10-101-464A-10	Sequence 10, Appl
44	130.6	6.7	564	4	US-10-101-464A-359	Sequence 359, App
45	130.6	6.7	567	4	US-10-101-464A-189	Sequence 189, App

ALIGNMENTS

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RESULT 1
US-09-602-472A-1
; Sequence 1, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Hu, Xu
; APPLICANT: Li, Guihua
; TITLE OF INVENTION: Sunflower Disease Resistance Genes
; FILE REFERENCE: 35718/200630
; CURRENT APPLICATION NUMBER: US/09/602,472A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/140,876
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
US-09-602-472A-1

Query Match          9.9%; Score 192.8; DB 4; Length 1593;
Best Local Similarity 57.4%; Pred. No. 1.7e-41;
Matches 410; Conservative 0; Mismatches 292; Indels 12; Gaps 3;

QY 784 ACTTCACATACAGAGAGCTAGAGCCCAATGTTCTCCGAGCGAATTGTTA 843
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Db 226 AATTCACTTCCTCGGAGCTTCAGCTGCACAAACAAATTAGCCCTATTGTTGCTA 285

QY 844 GGACAAAGCGGCTTGCTTACGTGCACAAAGGTGTTGCTT---AGTGGAAAGAGTT 900
   |||||
Db 286 GGAGAAAGGAGGCTTGGCCATGTATAGAGGACGGCTTCGCGACGCTCAGATTGTA 345

QY 901 GCTTGGAAGCAATTGAAGTTGGAGTGTTCAGGGAGAGAGAGTTTCAGGAGAGTT 960
   |||||
Db 346 GCTTGCAACCAATTGGATAGGAACGGGCTGCAGGGGTAACCGTAATTTCTCGTAAGATT 405

QY 961 GAGATCATCAGAGAGATTCCACCAAGGCAATCGTGTCTCTTGTGTTATGATGATGCC 1020
   |||||
Db 406 CTTATGCTCAGCTTTTACATCATCCCAATTTGGTAATTTAATGGATACGTGCTGAT 465

QY 1021 GGTGCAAAAGATTGCTTCTATGAGTTTGTCTTAACAACATTCGAGCTTACCTC 1080
   |||||
Db 466 GGTGCAAAAGCTTCTGTTTATGATTCATGCGCCATTGGGATCGTTAAAGATCACTT 525

QY 1081 CATGGGAGGAGCGGCGCTA-----CAATGATGAGGAGCAGAGATTGAAGTGTGCTT 1134
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Db 526 CATGATCTCCACCGAGAAAAGAGCGTTAGATTGGAACACAGATGAAGATTAGCGGCT 585

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QY 1135 GGATCTGCTAAGAGACTTTCTTATCTCATGAGATTGCANCTAAATCATTCACCGT 1194
Db 586 GGTGACGTGACAGGTTTGGAATTTCTTACGTAAGGTAATCTCCCTGTTATTTACAG 645
QY 1195 GATATCAAGGCTTCAACATATATGATGATTTCAGATTTCAGAGTTGCTGATTTT 1254
Db 646 GATTTCAAATATCAAAACATTTTGTCTCGTAGGGATTTCAACCAACCTTTTCATTTT 705
QY 1255 GGTCTGTGTAGATTG---CTTCTGATACAAACGCGATATGATCAACGCGTGTATGGGA 1311
Db 706 GGGCTAGGAGATTGGGCGCCGACGGAGATAGTCTCATATGATCCACGCGTCA795GA 765
QY 1312 ACCTTTGGGTAAGTCTGCTCCGGAATACGCTGCAAGCGGAAGCTTCACGGAAGTCTGAC 1371
Db 766 ACGATAGTACTGCTGCTCGTAGATGCGATGACCGGATCAACTGATTAACTGAT 825
QY 1372 GTTTTCTATTGTTGGGCTGTGCTTTGGAGCTCATTTACTGACGTCGACCGCTGATGCC 1431
Db 826 GTGTATAGCTTTGGGCTGTGTTTCTTAAAGCTTATTAACGCGCGAAAGCCATTGACAGC 885
QY 1432 AACATGCTATGATGATGACAGCTTATGATGCTGGGACGACCATTTGCTTAA 1485
Db 886 AGTGACCGCAGAGACAGACAGATCTGCTCACTTGGGACAGACCTTATTCAAC 939

RESULT 2

US-10-101-464A-886
Sequence 886, Application US/10101464A
Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101,464A
PRIOR FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 886
LENGTH: 3108
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-10-101-464A-886

Query Match 9.9%; Score 192.4; DB 4; Length 3108;
Best Local Similarity 53.9%; Pred. No. 3.2e-41;
Matches 419; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

QY 787 TTCACATACGAGAGCTAGTAGAGCCACCATGTTTCTCCGAGGCAACTGTTAGGA 846
Db 1881 TACCATTACGGCGCATTTGAAGAGGCTACGAATATTTTAAGGAAGATTGATTAATAGG 1940
QY 847 CAAGCGGGGTTGGTTAGCTGACAAAGTGTTGCTCAGTAGGAAGAAGTTGCTGTG 906
Db 1941 ACGGAGGTTTGGGAAAGGCTTACAAAGGAATTTTCAAGATGGAGCTAAAGTGCAGTG 2000
QY 907 AAGCAATTGAAGTTGGAGTGTCAGGAGAGAGAGAGAGGATTTCAGGACAGGTTGAGTC 966
Db 2001 AAGAGGGGCAATCCAAAGTCCCAACAGGGGCTGACGGAGTTCCGTAACGAATCGAGATG 2060
QY 967 ATCAGCAGAGTTTACCAAGGCAATGCTGTCTCTTGTGTATGATGCGCGGTGCC 1026

Db 2061 TTGCTCAGTTTCGACCCGCCATCTGATGCTGATCCGGTATTTGCAAGCAAGAAAT 2120
QY 1027 AAAAGATTGCTGTGCTATGAGTTTGTCTTACAAACAATCTCGAGCTTCACTCCATGAGC 1086
Db 2121 GAGATGATCATCATCTATGAATTTATGAGAAACGGGACCTTAAGATGATCTGTACTGT 2180
QY 1087 GAGGACGGGCTTACATGGAATGAGACCAAGATTGAAGATTGCTCTTGAATCTGCTAAA 1146
Db 2181 TCGGATGCTCCGTCGATGAGTTGGAAGCAAAAGCTGAGATTGTCATTTGGGTCAGCTAAA 2240
QY 1147 GGACTTTTATTTCTTCAAGAAATTTGCAATCTTAAATCATTCACCGTATATCAAGCT 1206
Db 2241 GGGCTTCACTAACCTTCAACCGGCTCCACAAAGGCAATCATTCATCCGAGCTCAAGTCG 2300
QY 1207 TCAACATATTGATAGATTTCAGATTGAAGCTAAGTTGCTGATTTGTCTGCTGAAG 1266
Db 2301 GCAATATCTCTTTGATGAGAAATTTGATGCGCAAGTTGCCGATTTGGGCTGCAAG 2360
QY 1267 ATTGCTTGTATACAAAC--ACGATGATATCAACAGTGTGATGGAACTTTGGGTAC 1323
Db 2361 ACCGCTCTGAGATGACACAGACGACGTCAGACAGCCGTGAAGAGGAGCTCGGATAT 2420
QY 1324 TTGGCTCCGGAATACGCTGCAAGCGGAAAGCTACGAGAGATGCTGATCTTCTCATTT 1383
Db 2421 CTGATCTGAATACCTGACGAGGACAGCTCACGGAAATATCATGATCTACTCATTT 2480
QY 1384 GCGCTGTGCTTTTGGAGCTCATTTACTGACGCTGACCGCTGTGATCCCAATGCTAT 1443
Db 2481 GGGGCTGATGCTTGAATCTCTTTGTGTAGACGGTATTCGATCCGCTGCCAGCA 2540
QY 1444 GTAGATGACAGCTTAGTTGACTGGGACGACCATTTCTTAAACGAGCATCTGAGCAAGA 1503
Db 2541 GAAAGGGAATTTAGTTGAGTGGGCAATGAAATGGCGCAGAAAGGCGGAATCCAAAGA 2600
QY 1504 GACTTGAAGGTTTAGCTGATGCAAAAGATGAATATGCTATGACAGAGAGAGATGG 1561
Db 2601 ACCATTAAGCCTCATCTTGTGGCTCAAGCAAGTGAAGTCCCTCTGGAAGTTGCTGG 2658

RESULT 3

US-09-228-986-4
Sequence 4, Application US/09228986
Patent No. 6359198

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 2868
TYPE: DNA
ORGANISM: Pinus radiata
US-09-228-986-4

Query Match 9.4%; Score 182; DB 3; Length 2868;
Best Local Similarity 52.9%; Pred. No. 1.9e-38;
Matches 467; Conservative 0; Mismatches 400; Indels 15; Gaps 3;

QY 787 TTCACATACGAGAGCTAGTAGAGCCACCAATGTTTCTCCGAGGCAACTGTTAGGA 846
Db 1116 TTTCATTACGGGAATTACAGTTGCCAATGATGTTTATAGCAATAGAAACATTTCTTGGC 1175
QY 847 CAAGCGGGGTTGGTTAGCTGACAAAGTGTTGCTCTAAGTGGAAAGAAAGTTGCTGTG 906
Db 1176 AAGAGTGTTTGGAAAGGTATACAAAGGGGCTTGGACAGATGTTCTTGGTGGCTGTA 1235
QY 907 AAGCAATTGAAGTTGGAGTGTCAG--GGAAGAGAGAGTTTCAGGCAAGAGTTGAG 963

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Db      1236 AACGCTGTAAGGAAGAGCGTACACCGGGTGGAGAGTTGCAAGTTTCAACAGAAATGGAG 1295
Qy      964 ATCATCAGCAGAGTTTACACCAAGAGCATGGTGTCTTGTGTGTATTTGATGACCGCGT 1023
Db      1286 ATGATAGCATGCGAGTACATAGGAACCTCTTGCACATACGGATTTCTGATGACACCC 1355
Qy      1024 GCCAAAGATTGCTGTCTATGAGTTTGTCTTAACAACAATCTGAGCTTCACTTCAT 1083
Db      1356 ACTGAACCGCTGCTGTATTTATCCATACATGGCCATGGAAGTTGCTTCAAGCTTACGA 1415
Qy      1084 GCGCAGGAGC-----GGCCTAACAATGGAATGAGACCAACAATTGAAGATTGCTTGGGA 1137
Db      1416 GAGAGGACCAAAATGACCCACCTTAATTTGGCCAACTCGACACGCAATGATGGAT 1475
Qy      1138 TCTGTAAGAGACTTTCTATCTTCATGATGAAATGCAATCTTAATATCATTCACCGTAT 1197
Db      1476 TCTGTAAGAGCTCTCTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1535
Qy      1198 ATCAAGGCTTCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
Db      1536 GTCAAGGCTGCTAATCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1595
Qy      1258 CTGCTAAGATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db      1596 TTGCAAAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1655
Qy      1318 GGGTACTTGGCTCCGGAATAGCGTCAAGCGGAAGCTCAACGAGAGTCTGACGTTTTC 1377
Db      1656 GCGCAATAGACACCTGAGTACCTTTCTATGATGATGATGATGATGATGATGATGATGATGAT 1715
Qy      1378 TCATTTGCGGTTGCTTGTGAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
Db      1716 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1769
Qy      1438 GTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db      1770 GACGTTTATGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1829
Qy      1498 CAAGAGACTTTGAGGTTTATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
Db      1830 GAGAAAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1889
Qy      1558 ATGCTCGATGCTGCTTGTGAGTCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
Db      1890 GTGGAACAATCTTATCAAGTTGCTTATCTTATGATGATGATGATGATGATGATGATGAT 1949
Qy      1618 CGCATGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1659
Db      1950 AAGATGCTGAAGTGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991

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RESULT 4
US-10-101-464A-4
; Sequence 4, Application US/10101464A
; Patent No. 678041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-4
Query Match      9.4%; Score 182; DB 4; Length 2868;
Best Local Similarity 52.9%; Pred. No. 1.9e-38;
Matches 467; Conservative 0; Mismatches 400; Indels 15; Gaps 3;

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Qy      787 TTGATATACAGAGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
Db      1116 TTCTATTAACGGAATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1175
Qy      847 CAAGCGGCTTGGTTACGTCACAAAGGTTGTTGCTTACGATGATGATGATGATGATGATGATGATGAT 906
Db      1176 AGAGTGTGTTTGGAAAGGTGACAAAGGCGCTTGCAGATGATGATGATGATGATGATGATGATGAT 1235
Qy      907 AAGCATGAAAGTTGGAGTGTGAG---GAGAGAGAGGAGTTTCAAGCAGAGGTTGAG 963
Db      1236 AACGCTGTAAGGAAGAGCGTACACCGGGTGGAGAGTTGCAAGTTTCAACAGAAATGGAG 1295
Qy      964 ATCATCAGCAGAGTTTACACCAAGAGCATGGTGTCTTGTGTGTATTTGATGACCGCGT 1023
Db      1296 ATGATTAACATGAGCAGTACATGAGAACTCTTCACTACGATGATGATGATGATGATGATGAT 1355
Qy      1024 GCCAAAGATTGCTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
Db      1356 ACTGAACGCTGCTGTGTTTATCTTACATGAGCAATGAGATGATGATGATGATGATGATGATGAT 1415
Qy      1084 GCGCAGGAGC-----GGCCTAACAATGGAATGAGACCAACAATGGAATGATGATGATGATGAT 1137
Db      1416 GAGAGGCGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1475
Qy      1138 TCTGTAAGAGACTTTCTATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1197
Db      1476 TCTGTAAGAGCTCTCTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1535
Qy      1198 ATCAAGGCTTCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
Db      1536 GTCAAGGCTGCTAATCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1595
Qy      1258 CTGCTAAGATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db      1596 TTGCAAAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1655
Qy      1318 GGGTACTTGGCTCCGGAATAGCGTCAAGCGGAAGCTCAACGAGAGTCTGACGTTTTC 1377
Db      1656 GCGCAATAGACACCTGAGTACCTTTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1715
Qy      1378 TCATTTGCGGTTGCTTGTGAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
Db      1716 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1769
Qy      1438 GTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db      1770 GACGTTTATGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1829
Qy      1498 CAAGAGACTTTGAGGTTTATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
Db      1830 GAGAAAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1889
Qy      1558 ATGCTCGATGCTGCTTGTGAGTCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
Db      1890 GTGGAACAATCTTATCAAGTTGCTTATCTTATGATGATGATGATGATGATGATGATGATGAT 1949
Qy      1618 CGCATGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1659
Db      1950 AAGATGCTGAAGTGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991

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RESULT 5

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US-09-579-182-4
; Sequence 4, Application US/09579182
; Patent No. 650628
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: NMI-161
; CURRENT APPLICATION NUMBER: US/09/579,182
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-182-4

Query Match          9.2%; Score 179.8; DB 4; Length 1488;
Best Local Similarity 53.8%; Pred. No. 4.9e-38;
Matches 470; Conservative 0; Mismatches 382; Indels 21; Gaps 4;

QY 784 ACTTTCATACGAGGAGCTGAGGCCACCAATGGTTCTCCGAGCGAAGCTTTGA 843
DB 154 ACCTTTACTTCCGAGAGTTAGCTGCCGCACTAAAACCTTGCACCGGAATGCTTCTT 213
QY 844 GACACAGCGCGGTTCCGTTACGTCACAAAG---GTGTTGCTCTAGTGGAGAAAGATT 900
DB 214 GGAAGAGAGGTTCCGACGTTTACAAAGTGTCTAGAGACACACAGCAATAGTA 273
QY 901 GCTGTGAACAGTTGAAAGTTGGAGTGTGAGGAGAGAGAGAGTTTCAGGCAAGGTT 960
DB 274 GCTGTGAACAGTTGATCGAAGCGTCTACAGAAACAGAGAGTTCTGTGAGAGTT 333
QY 961 GAGATCATACGACAGATTACACAGAGCTGATGCTGCTGTTGTTATTTGATGCC 1020
DB 334 CTATGCTGAGCCTTCTGATCATCCCAATCTTGAAATTTGATTTGTTGCTGAT 393
QY 1021 GGTGCCAAAAGATTGCTGTCTATGAGTTGTTCTTAAACAATCTCGAGCTTCACTC 1080
DB 394 GGGAGCAGAGGCTTCTTGTGTATGAGTATATGCCACTAGATGATTTGGAGATCATCTA 453
QY 1081 CATGCCAGAGGAGCGGCTTA-----CATGGAATGAGACACAGATGGAATGCTCTT 1134
DB 454 CACGATCTTCCACTGATTAAGAGCCTCTAGACTGAGTACTAGAAATGACAAATGCGCA 513
QY 1135 GGAATCTGTAAGGACTTTCTATCTCATGAGAAATTTGCAATCTTAATATTCACCGT 1194
DB 514 GGAGCAGCAAGGAGCTGAGATATCTGATGATTAAGGAAATCGCCTGTGATCTACAGA 573
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QY 1312 ACCTTTGGATCTGCTGCGGAGTACGCTGCAAGCGGAAAGCTCAAGGAGAAATCTGAC 1371
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QY 1372 GTTTTCTCATTTGGCGTGTGCTTTTGAAGTCAATTAAGTACGCTGCAAGCGTGTATGCC 1431
DB 754 GTTATATAGCTTTTGGGTTGTGTTCTCGAGCTATCAAGGCTGAAAAGCATTTGATAT 813
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QY 1492 TCTGAGCAGAGAGACTTTGAGGTTTATGCTGATGCAAAAGATGAATATGAGTATGACAGA 1551
DB 867 --AGATGCTGTAAGAAAGTTTCCGAAGATGCGGATCATGCTGCAAGGCGGTTATTCATG 924
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US-09-228-986-9
; Sequence 9, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 3239
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-9

Query Match          9.2%; Score 178.4; DB 3; Length 3239;
Best Local Similarity 55.9%; Pred. No. 1.8e-37;
Matches 360; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

QY 1552 GAGAGATGCTGCATGATGTTGTTGCTGCGGCTTGTGTCGCCATGAGCTGCGGC 1611
DB 925 CGTGTCTATATCAAGACACTTTCAGTTCGACGCAATGTGTTTACAGAAACAAAGCAGCACA 984
QY 1612 AGACCTGCATAGACCCAGATTTGCGTGCCTTA 1644
DB 985 AGACCACATGATTTGCGACGTTGTGACAGCTCTTA 1017

RESULT 6
US-09-228-986-9
; Sequence 9, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 3239
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-9

Query Match          9.2%; Score 178.4; DB 3; Length 3239;
Best Local Similarity 55.9%; Pred. No. 1.8e-37;
Matches 360; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

QY 787 TTCATATACGAGAGCTAGCTAGAGCCACCAATGTTTCTCCGAGCGCAAGCTTTGTAGA 846
DB 2026 TTCTCTATATGATGAACTTAAGAGGTGACCAATATATTTCTCCGATAGCAATGAATTAGGC 2085
QY 847 CAAGCGCGGTTGCGTTACGTGACAAAGGTGTGCTAGTGGAGAAAGAGTTGCTGTG 906
DB 2086 TTGCGAGAGATACGAAAGGTGTACAGGAGAGTTCTTCTGATGTCTATATTTAGCAATC 2145
QY 907 AAGCATTTGAAAGTTGGAGTGTGTCAGGAGAGAGGAGATTTCAGGACAGAGTTGAGATC 966
DB 2146 AAAAGACTCAGACAGGAGGTGATGACAGGTCAGGTCACGAGTTCAAGACAGAAATGAGCTG 2205
QY 967 ATGACGAGTATCCACACAGGATCTGTGTCTTGTGTTATTTGCTATGTCATGCGGTC 1026
DB 2206 CTTTCGGGGTTATCAAGAAATCTTGTGGCTCATAGATTTCTGTTCGAGCAAGA 2265
QY 1027 AAAAGATTGCTGTCTATGAGTTGTTCTTAACAACAATCTCGAGCTTCACTCCATGCG 1086
DB 2266 GAGGAGATTTGCTATGATATATATGCTTACGAGGAGCTCAAGGATAGCTTGACAGGA 2325
QY 1087 GAGGAGCGGCTTACATGATGAGTGAAGACCAAGATTTGAAGATTTGCTTGAATCTGCTAAA 1146
DB 2326 AAATCAGGACTTTATCTTGAATTTGGAAGAGAGGCTTGATAGCTTACGTTGCGCTAGA 2385
QY 1147 GGAATTTCTTATCTTCAATGAAATTTGCAATCTTAAATCATTTACCGTGATATCAAGGCT 1206
DB 2386 GGAATTAATTTATCTGACGAATCTCGCAATCTTCAATTTATCCACAAGAGATGTCAGAGCTC 2445
QY 1207 TCAAAATATTTGATATGATTTCAAGTTTGAAGCTTGAAGTGTGCTGTTGCTTGTCTGAAG 1266
DB 2446 ACCAATATCTTGTGTGACGAACATCTAGACGCGCAAAATCGCGATTTTCGTTTGTCCAAA 2505
QY 1267 ATTGCTTGTGATA---CAAAACGATGATTAACACGCTGTGATGGAACCTTTGGGTAC 1323
DB 2506 CTGTTATCGACAGCGGAGAGGAGGACAGCTTTCGACGAAAGTGAAGGACAGCTGGCTAT 2565
QY 1324 TTGCTCCGGAATATGCTGCAAGCGGAAGCTCAAGGAGAGTGTGAGCTTTCTCATTT 1383
DB 2566 TTGATCTCCGAATATCTATGATGATCAACAGCTGACAGAAAGAGCGATGTGTACAGCTTC 2625
```


QY 1384 GGCCTTGCTTTGGAGCTCACTAGAGCTCGACCCGTTGA 1427
 Db 2626 GGGGTGTCATGCTTGAAGCTCATCACTGCAAGAACCGATTGA 2669

RESULT 7
 US-10-101-464A-9

; Sequence 9, Application US/10101464A
 ; Patent No. 6768041
 ; GENERAL INFORMATION:
 ; APPLICANT: Strabala, Timothy
 ; APPLICANT: Nieuwenhuizen, Nicolaas
 ; APPLICANT: Higgins, Colleen M.
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells
 ; FILE REFERENCE: 11000.1020C2
 ; CURRENT APPLICATION NUMBER: US/10/101,464A
 ; PRIORITY FILING DATE: 2002-03-18
 ; PRIORITY FILING DATE: 09/704,302
 ; PRIORITY FILING DATE: 2000-11-01
 ; PRIORITY FILING DATE: 09/228,986
 ; PRIORITY FILING DATE: 1999-01-12
 ; PRIORITY FILING DATE: 60/162,866
 ; PRIORITY FILING DATE: 1999-11-01
 ; PRIORITY FILING DATE: PCT/US00/00724
 ; NUMBER OF SEQ ID NOS: 989
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 3239
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 ; US-10-101-464A-9

Query Match 9.2%; Score 178.4; DB 4; Length 3239;
 Best Local Similarity 55.9%; Pred. No. 1.8e-37;
 Matches 360; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

QY 787 TTCACATACGAGAGCTAGTAGACCAACCAATGGTTTCCGAGCGCACTTTGAGGA 846
 Db 2026 TTCTCTATGATGAACTTAAGAGGTGACCAATATTTCTCCGATAGCAATGAATTTAGGC 2085
 QY 847 CAAGCGGCTTGGTTACGTGCAAAAGGTGTGCTTCTGCTTGAAGAAAGTTGCTGTG 906
 Db 2086 TTCGAGAGTACGAAAGGTGTACAGGGGAGTTCTTCCGATGCTCATATTTAGCAATC 2145
 QY 907 AAGCATGGAAGTTGGAGGTGTGAGGAGAGAGAGAGTTTCAGGCAAGTTGAGATC 966
 Db 2146 AAAAGAGCTCAGAGGGGTGATGAGGAGGTGCAACCGAGTTCAAGCAAAATGAGCTG 2205
 QY 967 ATCAGCAGAGTTCCACCAAGAGCTGTGTCTTTGTTGTTTGTGATTCGCGGATGCG 1026
 Db 2206 CTTTGGCGGTTCATCAGAGATCTGTGTGGCTTCATGAGATCTGTTTCCAGCAAGA 2265
 QY 1027 AAAAGATGCTTGTCTATGAGTTGTCTTAAACAACATCTGAGCTTCACTCGATGCG 1086
 Db 2266 GAGCAGAGTGTGTCTATGATATATATGCTTAAAGGAGCTCAGGAGATGCTTGA 2325
 QY 1087 GAGGAGCGGCTTACAGATGGAATGAGGAGCAAGATTTGAAGATGCTTGGATCTGTAA 1146
 Db 2326 AATATGAGCATTTATCTTATGATGAGAGAGAGAGCTTCTGATAGCTTGAAGTTGCGCTAA 2385
 QY 1147 GACATTTCTTATCTTATGATGAGATGCAATCTTAAATCATTCACCGTATTCAGAGCT 1206
 Db 2386 GAGACTAGCTTATCTGAGCAAGCTCGGATCTTCCATATATCAGAGATGCTCAAGTTC 2445
 QY 1207 TAAACATATTTATGATTTCAAGTTGAAGTTGAAGTTGCTGATTTGGTCTTGTAA 1266
 Db 2446 ACCAATATCTTGTGAGCAGACATGAGCGCAAGTGTGCGATTTGGTTGTCAAA 2505
 QY 1267 ATTGCTTCTGATA---CAAAACGATGATATCAACGTTGAGGAACTTTGGGTAC 1323

Db 2506 CTGGATATGACAGCGGAGAGGAGCAGTTTCAGACGAATGGAAGGCAAGCTGGGCTAT 2565
 QY 1324 TTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCAGGAAAGTTGAGTTTTCATTT 1383
 Db 2566 TTGATTCGGAATATCTATGATGATGATCAACAGCTGACAGAAAGAGGATGTGTACAGCTTC 2625

RESULT 8
 US-09-602-472A-3

; Sequence 3, Application US/09602472A
 ; Patent No. 6608240
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Hu, Xu
 ; TITLE OF INVENTION: Sunflower Disease Resistance Genes
 ; FILE REFERENCE: 35718/200630
 ; CURRENT APPLICATION NUMBER: US/09/602,472A
 ; PRIORITY FILING DATE: 2000-06-23
 ; PRIORITY FILING DATE: 60/140,876
 ; PRIORITY FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1559
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (81)...(1319)
 ; US-09-602-472A-3

Query Match 9.1%; Score 176.4; DB 4; Length 1559;
 Best Local Similarity 55.7%; Pred. No. 4.1e-37;
 Matches 402; Conservative 0; Mismatches 311; Indels 9; Gaps 3;

QY 773 TCTCAAAAGCACTTTCATCATGAGAGCTAGTAGAGCCCAATGGTTTCTCGAGG 832
 Db 280 TCGCCGCAAACTTCACATTCGCGAGCTGACGCGCCACCAATATTTTCAGCTTG 339
 QY 833 CGAATTTGTAAGAAAGCGGCTTCCGTTACGTCACAAAG---GTGTGTTCCCTAGTG 889
 Db 340 ATTGCTTTTAAGGAGAGGTTGTTTGTGTATATAGAGAGCTCTTCAAGATAGTG 399
 QY 890 GGAAGAAGTTGCTGTGAAGCACTTGAAGATTTGAGAGTGTGCAAGAGAGAGAGTTTC 949
 Db 400 GTCAAGTTGTATGCTTTTAAACAGCTGATGAAATGACTCCAGGTAAACCTGAGATTTC 459
 QY 950 AGGCAAGTTGAGATGATCATGAGCAAGATTTCAACAGAGCATGCTGTGTTGTTGTT 1009
 Db 460 TTGTGAAGTTCTTATGCTCAGCTTTTATCATCATCAACCTGTGCAATTTGATTTGCT 519
 QY 1010 ATTGATGCGCGGTCGCAAAAGATTTCTGTCTATGATGTTGTTCTTCAACAATCTCG 1069
 Db 520 ACTGCGTGAAGGTGATCAAGAGCTCTTGTGTATGAGTTTATGCTTGGGTTCTTGG 579
 QY 1070 AGCTTCACTTCATGAGCGAGAGAGCGCTTACATGAGATGAGACACAGATTTGAAGATTG 1129
 Db 580 AAGATCACCTTCATATGATTTCCGCTGACAGAAACATTTAGATGAGACAGAGATGAG 639
 QY 1130 CTCTTGAT---CTGCTAAAGAGCTTTCTTATCTTCATGATGAGATGCAATCTTAAATGA 1186
 Db 640 ATAGCGCTGTGACAGCAAGAGGTTGAGTTCTTCTATATTAAGTTAAACCAACAGCTTA 699
 QY 1187 TTCACGATGATTAAGAGCTTCAACATATTTGATGATTTCAAGTTTGAAGCTTAAGTTG 1246
 Db 700 TTTATCGGAGCTTCAATCATCAACATTTTCTGATGATGAGGATTTTCAACCAAGCTGT 759
 QY 1247 CTGATTTTGTCTTGTGAAGATTGCTTCTGATTAACAGC---CATGATTAACAGCTG 1303

Db 760 CCGACTTCGGGCTCGCGAAGCTGGGCCCCACTGGAGAGCAAGCTTCATGTTCCACAGCGG 819
QY 1304 TGAATGGGACCTTTGGGACTTGGCTCCGGATACGCTGCAAGGGAAGCTCACGAGAGA 1363
Db 820 TGAATGGGACCTTTGGGACTTGGCTCCGGATACGCTGCAAGGGAAGCTCACGAGAGA 879
QY 1364 AGCTGACGCTTTTCTCATTTTGGGCTTGGCTTTGGAGCTCATTAAGTGAAGCTGCAAGCGG 1423
Db 880 AATCCGATGCTACAGCTTGTGTGCTTTTGGAGCTTATTAACGGTGAAGAAAGCA 939
QY 1424 TTGATGCCACAAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCAAGCAATGTCTTA 1483
Db 940 TAGATAGACTCAACCAACATGAGACAGAGAACTGTGTACATGGGCAAGCTTGTCTTA 999
QY 1484 AC 1485
Db 1000 AC 1001

RESULT 9
US-09-228-986-7
; Sequence 7, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2432
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-7

Query Match 9.0%; Score 174.6; DB 3; Length 2432;
Best Local Similarity 56.5%; Pred. No. 1.6e-36;
Matches 368; Conservative 0; Mismatches 274; Indels 9; Gaps 2;
QY 787 TTCACATACGAGAGCTAGTAGAGCCACCAATGGTTCTCCGAGCGAAGCTTTAGGA 846
Db 1070 TTCTCATTAAGAGGTTACGTTTCCACTATATTTTACTAGCAGAAATATTTTAGA 1129
QY 847 CAAGCGGCTTGGTTACGTGCACAAAGGTGTGCTTACTGTGGAAAGAGTTGCTGTG 906
Db 1130 GTAGAGAGATATGATTTGTCTATTAAGGATTCTTAAGATGGCACTATATGTAGCAATA 1189
QY 907 AAGAGTTGAAGTTGGAGT---GTCAGGAGAGAGGAGTTTCCAGGAGAGTTGAG 963
Db 1190 AAAAGTTGAAGATGTAATGTGTGAGAGAGAGAAATTCATTTCAAAACAGAGTGA 1249
QY 964 ATCATACGAGAGTTCAACCAAGCAATCTGTGTCTCTTTGGTTATTTGATGCCGGT 1023
Db 1250 ATGATACGCTTGGCTGTGCAATAGAACTTATAGATTTGATTTTGGACAACTCC 1309
QY 1024 GCCAAAAGATTGCTTGTCTATGAGTTGTTCTTAACAACAATCTCG-----AGCTTAC 1077
Db 1310 AGAGAGAGGCTTCTGTCTATCCCTACATGCAATGGAATGTGTGCTTGTCTTGA 1369
QY 1078 CTCATGGCGGAGGAGCGGCTCAATAGATGAGACCAATGGAATGATTTGCTTGA 1137
Db 1370 GATCATTTAATGGAAGAGCTTCCCTGAGCTTGGCTTACGCAAGCGTATAGCTTTGA 1429
QY 1138 TCTCTAAGAGCTTTCTTATCTTCAATGAAGTTGCAATCTTAATCAATTTACCGTGAT 1197
Db 1430 GCGAGTGGGAGCTGTTATATTTTGCATGAGCAATGTATCCCAAGATTTATCACCGGAT 1489
QY 1198 ATCAAGGCTTCAACATATTTAGATTTCAAGTTTGAAGCTAAGTTGCTGATTTGGT 1257

Db 1490 GTGAAGAGAGAAATATATTACTGATGAATATTTTGAAGCTGTGTGGAGATTTGGG 1549
QY 1258 CTCTCTAAGATTTGCTTGTGATCAAAACGCAATGATATCAACAGTGTGATGGAACTTT 1317
Db 1550 TTACAAAGCTTCTTGATACAGAGGATTTCTATGTACTACTGTCTTCCAGGAGCGGTA 1609
QY 1318 GGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGAGAAAGTCTGAGCTTTTC 1377
Db 1610 GGTCAATTTGCCAGAAATACCTTTCAACGAGCAATCTTCAAGAAACCTGATGATTT 1669
QY 1378 TCATTGGCGCTTGTGCTTTTGGAGCTCATTAAGTGAAGCTGCAAGCGGTTGAT 1428
Db 1670 GCGTTGGAAATATTACTGTTGGAATCTATTAACAGCAAAAGGCTTTAGAT 1720

RESULT 10
US-10-101-464A-7
; Sequence 7, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2432
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-7

Query Match 9.0%; Score 174.6; DB 4; Length 2432;
Best Local Similarity 56.5%; Pred. No. 1.6e-36;
Matches 368; Conservative 0; Mismatches 274; Indels 9; Gaps 2;
QY 787 TTCACATACGAGAGCTAGTAGAGCCACCAATGGTTCTCCGAGCGAAGCTTTAGGA 846
Db 1070 TTCTCATTAAGAGGTTACGTTTCCACTATATTTTACTAGCAGAAATATTTTAGA 1129
QY 847 CAAGCGGCTTGGTTACGTGCACAAAGGTGTGCTTACTGTGGAAAGAGTTGCTGTG 906
Db 1130 GTAGAGAGATATGATTTGTCTATTAAGGATTCTTAAGATGGCACTATATGTAGCAATA 1189
QY 907 AAGAGTTGAAGTTGGAGT---GTCAGGAGAGAGGAGTTTCCAGGAGAGTTGAG 963
Db 1190 AAAAGTTGAAGATGTAATGTGTGAGAGAGAGAAATTCATTTCAAAACAGAGTGA 1249
QY 964 ATCATACGAGAGTTCAACCAAGCAATCTGTGTCTCTTTGGTTATTTGATGCCGGT 1023
Db 1250 ATGATACGCTTGGCTGTGCAATAGAACTTATAGATTTGATTTTGGACAACTCC 1309
QY 1024 GCCAAAAGATTGCTTGTCTATGAGTTGTTCTTAACAACAATCTCG-----AGCTTAC 1077
Db 1310 AGAGAGAGGCTTCTGTCTATCCCTACATGCAATGGAATGTGTGCTTGTCTTGA 1369
QY 1078 CTCATGGCGGAGGAGCGGCTCAATAGATGAGACCAATGGAATGATTTGCTTGA 1137
Db 1370 GATCATTTAATGGAAGAGCTTCCCTGAGCTTGGCTTACGCAAGCGTATAGCTTTGA 1429

QY 1138 TCTGCTAAGAGACTTCTTATCTTCATGAGAGATGCAATCCTTAATCATACCGGTAT 1197
 DB 1430 GCAGCTAGGGAGCTGTATATTTGATGATGAGCATGTGATCCCAAGATATATTCACCGGAT 1489
 QY 1198 ATCAAGGCTTCAACATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1257
 DB 1490 GTGAAGAGAGCAATATATTTACTGATGATGATGATGATGATGATGATGATGATGAT 1549
 QY 1258 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
 DB 1550 TTGAAGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609
 QY 1318 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
 DB 1610 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1669
 QY 1378 TCAATTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
 DB 1670 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1720

RESULT 11

US-10-101-464A-159
 ; Sequence 159, Application US/10101464A
 ; Patent No. 6768041
 ; GENERAL INFORMATION:
 ; APPLICANT: Strabala, Timothy
 ; APPLICANT: Nieuwenhuizen, Nicolaas
 ; APPLICANT: Higgins, Colleen M.
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells
 ; FILE REFERENCE: 11000.1020C2
 ; CURRENT APPLICATION NUMBER: US/10/101,464A
 ; PRIOR FILING DATE: 2002-03-18
 ; PRIOR APPLICATION NUMBER: 09/704,302
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/228,986
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/162,866
 ; PRIOR FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/00724
 ; PRIOR FILING DATE: 2000-01-11
 ; NUMBER OF SEQ ID NOS: 989
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 159
 ; LENGTH: 1457
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 ; US-10-101-464A-159

Query Match 8.9%; Score 173; DB 4; Length 1457;
 Best Local Similarity 55.6%; Pred. No. 3.2e-36;
 Matches 354; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

QY 784 ACTTTCATACATAGAGAGAGTAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
 DB 70 AATTTCAG 129
 QY 844 GAG 903
 DB 130 GAG 189
 QY 904 GTGAG 963
 DB 190 GTGAG 249
 QY 964 ATCATAG 1023
 DB 250 ATCATAG 309
 QY 1024 GCCAG 1080
 DB 310 CCTGAG 369

QY 1081 CATGCGAG 1140
 DB 370 GATGAG 429
 QY 1141 GCTAAG 1200
 DB 420 GCAG 489
 QY 1201 AAGGAG 1260
 DB 490 AAGGAG 549
 QY 1261 GCTAAG 1320
 DB 550 GCTAAG 609
 QY 1321 TACTGAG 1380
 DB 610 TATGAG 669
 QY 1381 TTGAG 1447
 DB 670 TATGAG 706

RESULT 12

US-10-101-464A-461
 ; Sequence 461, Application US/10101464A
 ; Patent No. 6768041
 ; GENERAL INFORMATION:
 ; APPLICANT: Strabala, Timothy
 ; APPLICANT: Nieuwenhuizen, Nicolaas
 ; APPLICANT: Higgins, Colleen M.
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells
 ; FILE REFERENCE: 11000.1020C2
 ; CURRENT APPLICATION NUMBER: US/10/101,464A
 ; PRIOR FILING DATE: 2002-03-18
 ; PRIOR APPLICATION NUMBER: 09/704,302
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/228,986
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/162,866
 ; PRIOR FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/00724
 ; PRIOR FILING DATE: 2000-01-11
 ; NUMBER OF SEQ ID NOS: 989
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 461
 ; LENGTH: 2175
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 ; US-10-101-464A-461

Query Match 8.7%; Score 168.2; DB 4; Length 2175;
 Best Local Similarity 55.9%; Pred. No. 7.8e-35;
 Matches 364; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 780 AACGAG 839
 DB 968 AAG 1027
 QY 840 GTTGAAG 899
 DB 1028 GATTGAAG 1087
 QY 900 TGTGAG 956
 DB 1088 TGTGAG 1147
 QY 957 GGTGAG 1016

Db 1148 ACTGAGATGATGAGCTAGGGGAGCAGCAACCTTCTGGCTCTATGATTTGTAT 1207
QY 1017 GCCCGGTGCAAAAGATTGCTTGTCTATGAGTTTGTCTTAAACAATCTGAGCTTCA 1076
Db 1208 GACCCAAACGGAGAGCTTCTGTATACCCCTACATGTCACAGGAGTGTGCACTG 1267
QY 1077 CCTCATGCGGAGGAGCGGCTTACATGAGATGAGCACAATGAGATTGCTCTTGG 1136
Db 1268 TCTCAGAGCCAA-----ACCAACCTTGAAGTGGAGCACAAGAAAAGATTGCTTGG 1321
QY 1137 ATCTGCTAAGGACTTCTTATCTTCATGAGATTGCAATCTTAAATCATTCACCTGA 1196
Db 1322 GCGAGCAAGGAGCTTGTGATCTGACAGCAATGTGACCCCAAAATATCATAGGGA 1381
QY 1197 TATCAAGCTTAAACATATGATATGATTTCAAGTTGAAGTGAAGTGTGCTTGG 1256
Db 1382 TGTTAAGGCGGAGACATATGCTTACACGACTACGGAAGCTGTGTGGAGACTTTGG 1441
QY 1257 TCTTGCTAAGTATGCTTGTGATACAAACAGCATGTATCAACAGCTGTGATGGAACTT 1316
Db 1442 ATTGCAAGCTTGTGATCATGAGGAAATCCACGTGACCAACCGCGTGAAGGAGCAGC 1501
QY 1317 TGGGTAATGCTGCTCCGAAATAGCTGCAAGCGGAAAGCTTACGAGAACTTGAACCTTT 1376
Db 1502 AGGGACATGCTCTCAGAGTACCTGTAAGCGGAGCTCTCTGAGAAAAACGATGTTTT 1561
QY 1377 CTGATTGGCGTGTGCTTTTGAAGTCAATTAATGAGCGTCCGACCGCTTGA 1427
Db 1562 TGGGTTTGAATCTTCTGCTGCACTGATTAAGCTGAGAGCTCTTGA 1612

RESULT 13
US-08-265-628-1
Sequence 1, Application US/08265628
Patent No. 5821094
GENERAL INFORMATION:
APPLICANT: Roche/Stein, Steven J.
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison St. Suite 3400
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,628
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/959,945
FILING DATE:
APPLICATION NUMBER: US 07/847,564
FILING DATE: 03-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien Ph.D., Donald J.
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brassica napus
STRAIN: oleifera
INDIVIDUAL ISOLATE: W1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: S-locus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2574
PUBLICATION INFORMATION:
AUTHORS: GORING, DAPHNE
AUTHORS: ROTHSTEIN, STEVEN J.
TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A
TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES A
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749
US-08-265-628-1

Query Match 8 6%; Score 166.4; DB 1; Length 2749;
Best Local Similarity 56.4%; Pred. No. 2.7e-34;
Matches 352; Conservative 0; Mismatches 266; Indels 6; Gaps 2;

QY 796 GAGGAGCTAGCTAGAGCCCAATGCTTCTCCGAGGCAACTGTTAGAGACAGGCGG 855
Db 1558 GAAGCTGTGTCAAAAGCCCAAAATTTCTCAATGTAAACAACCTGGACAAGGTGT 1617
QY 856 TTCGTTACGTGCAAAAGGTGTGCTTCTAGTGGGAAAAGTCTCTGAGACGTTG 915
Db 1618 TTCGTTATGTTTAAAGGAGTATGATTACTGATGGGCAAAATTTGGTAAAGGCTA 1677
QY 916 AAGGTTGGAGGTGTAGAGGAGAGAGAGTTCAGGACAGGTTAGATCATCAGAGA 975
Db 1678 TCAAAAACGTCGTTCAAGGAGCTGTGAGTTTATGATAGATGATGATCGGAGG 1737
QY 976 GTTCACCACAGGATGTGTCTCTTGTGTTATGATGATGATGATGATGATGATG 1035
Db 1738 CTTCAGATATTAACCTGTCCGAATCTTGGCTGTGATGAGGACAGAGAGATG 1797
QY 1036 CTGTCTATGATGTTGTTCTTACACAAATCTGAGCTTCACTCCATG--CGAGGA 1092
Db 1798 CTGATATGATGATTTAGAAAATTTAAGCTCGATTTTATCTTTCGGAATTAACA 1857
QY 1093 CGGCTACAAATGAGATGAGACCAAGATGAGATGCTCTGATGCTTAAAGACTT 1152
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RESULT 14
US-08-881-706-1

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; Sequence 1, Application US/08881706
; Patent No. 6245969
; GENERAL INFORMATION:
; APPLICANT: Chong, Joane
; APPLICANT: Li, Jiaming
; TITLE OF INVENTION: Receptor Kinase BIN1
; FILE REFERENCE: 07251/022001
; CURRENT APPLICATION NUMBER: US/08/881,706
; CURRENT FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4104
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97) ..(3687)
US-08-881-706-1
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Best Local Similarity 55.4%; Pred. No. 4e-33;
Matches 382; Conservative 0; Mismatches 296; Indels 12; Gaps 3;
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; GENERAL INFORMATION:
; APPLICANT: Chory, Joane
; APPLICANT: Jiaming, Li
; APPLICANT: Salk Institute for Biological Studies
; TITLE OF INVENTION: RECEPTOR KINASE, BIN 1
; FILE REFERENCE: SALKINS.012CP1
; CURRENT APPLICATION NUMBER: US/09/823,394
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97) ... (3684)
US-09-823-394-1
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Best Local Similarity 55.4%; Pred. No. 4e-33;
Matches 382; Conservative 0; Mismatches 296; Indels 12; Gaps 3;
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 12:25:15 ; Search time 122 Seconds

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Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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137	17	0.9	219	4	US-09-248-796A-7282	Sequence 7282, Ap	210	17	0.9	1444	4	US-09-489-039A-2452	Sequence 2452, Ap
138	17	0.9	256	4	US-09-313-294A-2332	Sequence 2322, Ap	211	17	0.9	1464	4	US-09-612-402B-11	Sequence 11, Appl
139	17	0.9	258	4	US-09-248-796A-7564	Sequence 7564, Ap	212	17	0.9	1477	3	US-09-614-221A-165	Sequence 15, Appl
140	17	0.9	285	4	US-09-513-999C-8469	Sequence 8469, Ap	213	17	0.9	1494	4	US-09-123-030-9	Sequence 9, Appl
141	17	0.9	291	4	US-09-313-294A-4913	Sequence 4913, Ap	214	17	0.9	1496	4	US-09-212-529-1	Sequence 1, Appl
142	17	0.9	292	4	US-09-313-294A-6396	Sequence 6396, Ap	215	17	0.9	1496	4	US-09-404-570B-157	Sequence 157, Ap
143	17	0.9	320	4	US-09-023-655-159	Sequence 159, Ap	216	17	0.9	1499	4	US-09-900-672-1	Sequence 1, Appl
144	17	0.9	333	4	US-09-270-767-11304	Sequence 11304, A	217	17	0.9	1500	3	US-09-330-651-1	Sequence 1, Appl
145	17	0.9	349	3	US-08-688-988-46	Sequence 46, Appl	218	17	0.9	1572	4	US-09-489-039A-1399	Sequence 1399, Ap
146	17	0.9	369	4	US-09-489-039A-1400	Sequence 1400, Ap	219	17	0.9	1572	4	US-09-270-767-1002	Sequence 1002, Ap
147	17	0.9	383	4	US-10-101-464A-393	Sequence 393, Ap	220	17	0.9	1596	4	US-09-270-767-1002	Sequence 1002, Ap
148	17	0.9	414	4	US-09-252-991A-14714	Sequence 14714, A	221	17	0.9	1596	4	US-09-270-767-1002	Sequence 1002, Ap
149	17	0.9	417	4	US-09-252-991A-4871	Sequence 4871, Ap	222	17	0.9	1613	3	US-08-976-259-111	Sequence 11, Ap
150	17	0.9	420	4	US-09-814-915A-105	Sequence 105, Ap	223	17	0.9	1613	3	US-09-956-004-111	Sequence 17, Appl
151	17	0.9	444	4	US-09-248-796A-3435	Sequence 3435, Ap	224	17	0.9	1654	3	US-09-774-528-17	Sequence 17, Appl
152	17	0.9	481	3	US-09-387-212-14	Sequence 14, Appl	225	17	0.9	1654	3	US-09-416-050A-3	Sequence 3, Appl
153	17	0.9	481	4	US-09-948-802-14	Sequence 14, Appl	226	17	0.9	1654	3	US-09-665-309-3	Sequence 3, Appl
154	17	0.9	484	4	US-09-621-976-10165	Sequence 10165, A	227	17	0.9	1654	3	US-09-665-309-3	Sequence 3, Appl
155	17	0.9	489	3	US-09-199-637A-430	Sequence 430, Ap	228	17	0.9	1682	4	US-09-220-132-82	Sequence 82, Appl
156	17	0.9	543	3	US-09-248-796A-7493	Sequence 7493, Ap	229	17	0.9	1682	4	US-09-919-039-223	Sequence 23, Ap
157	17	0.9	549	4	US-08-851-190-2	Sequence 2, Appl	230	17	0.9	1738	4	US-09-566-921-76	Sequence 76, Appl
158	17	0.9	552	4	US-09-216-430C-3	Sequence 3, Appl	231	17	0.9	1794	3	US-08-123-357-45	Sequence 45, Appl
159	17	0.9	594	4	US-09-252-991A-4851	Sequence 4851, Ap	232	17	0.9	1794	3	US-09-252-991A-3938	Sequence 3938, Ap
160	17	0.9	609	3	US-09-328-081-315	Sequence 412, Ap	233	17	0.9	1794	4	PCT-US94-10080-9	Sequence 9, Appl
161	17	0.9	631	3	US-08-961-081-315	Sequence 35, Appl	234	17	0.9	1794	5	US-09-799-451-681	Sequence 681, Ap
162	17	0.9	631	4	US-09-536-784-35	Sequence 35, Appl	235	17	0.9	1849	4	US-09-774-528-334	Sequence 23, Ap
163	17	0.9	645	4	US-09-134-000C-1423	Sequence 1423, Ap	236	17	0.9	1849	4	US-09-465-558-35	Sequence 35, Appl
164	17	0.9	687	4	US-09-252-991A-2936	Sequence 2936, Ap	237	17	0.9	1951	4	US-09-227-357-45	Sequence 45, Appl
165	17	0.9	692	4	US-09-270-767-7516	Sequence 7516, Ap	238	17	0.9	2053	3	US-09-227-357-45	Sequence 45, Appl
166	17	0.9	692	4	US-09-270-767-22798	Sequence 22798, A	239	17	0.9	2061	4	US-09-252-991A-3938	Sequence 3938, Ap
167	17	0.9	726	3	US-09-171-517B-3	Sequence 3, Appl	240	17	0.9	2100	1	US-08-154-915-5	Sequence 5, Appl
168	17	0.9	768	1	US-08-236-918A-5	Sequence 5, Appl	241	17	0.9	2138	4	US-10-101-464A-462	Sequence 462, Ap
169	17	0.9	768	3	US-09-150-864A-5	Sequence 5, Appl	242	17	0.9	2170	4	US-09-801-861-1	Sequence 1, Appl
170	17	0.9	773	1	US-09-328-475C-164	Sequence 164, Ap	243	17	0.9	2203	4	US-10-224-562-1	Sequence 1, Appl
171	17	0.9	800	1	US-08-390-858B-35	Sequence 35, Appl	244	17	0.9	2203	4	US-09-252-991A-3884	Sequence 3884, Ap
172	17	0.9	803	1	US-08-390-858B-37	Sequence 37, Appl	245	17	0.9	2316	4		
173	17	0.9	822	3	US-09-228-986-38	Sequence 38, Appl	246	17	0.9				

C 247	17	0.9	2328	4	US-09-252-991A-3965	Sequence 3965, Ap	320	16	0.8	78	3	US-08-479-744A-36	Sequence 36, Appl
C 248	17	0.9	2347	5	PCT-US96-03965-1	Sequence 1, Appl1	321	16	0.8	78	3	US-08-280-757B-36	Sequence 36, Appl
C 249	17	0.9	2350	1	US-08-012-269A-1	Sequence 1, Appl1	322	16	0.8	78	4	US-09-227-595-5	Sequence 5, Appl
C 250	17	0.9	2370	1	US-08-104-072B-7	Sequence 7, Appl1	323	16	0.8	78	4	US-09-425-762-36	Sequence 36, Appl
C 251	17	0.9	2370	1	US-08-351-413-8	Sequence 8, Appl1	324	16	0.8	78	4	US-08-595-590B-5	Sequence 5, Appl1
C 252	17	0.9	2370	2	US-09-025-583-8	Sequence 8, Appl1	325	16	0.8	78	4	US-09-513-999C-31160	Sequence 31160, A
C 253	17	0.9	2372	4	US-09-023-655-1076	Sequence 1076, Ap	326	16	0.8	80	1	PCT-US91-03388-5	Sequence 5, Appl1
C 254	17	0.9	2457	4	US-09-919-497-42	Sequence 42, Appl	327	16	0.8	80	1	US-07-800-364B-5	Sequence 5, Appl1
C 255	17	0.9	2508	4	US-09-489-039A-1569	Sequence 1569, Ap	328	16	0.8	86	1	US-08-150-331-47	Sequence 47, Appl
C 256	17	0.9	2534	4	US-09-620-312D-80	Sequence 80, Appl	329	16	0.8	86	4	US-08-569-284-47	Sequence 47, Appl
C 257	17	0.9	2590	1	US-08-524-757-11	Sequence 11, Appl	330	16	0.8	90	4	US-09-792-024-347	Sequence 347, Appl
C 258	17	0.9	2690	4	US-09-556-877-170	Sequence 170, App	331	16	0.8	103	4	US-09-513-999C-11666	Sequence 11666, A
C 259	17	0.9	2849	4	US-09-620-412C-170	Sequence 170, App	332	16	0.8	149	4	US-09-513-999C-12888	Sequence 32888, A
C 260	17	0.9	2949	4	US-09-598-419-170	Sequence 170, App	333	16	0.8	183	4	US-09-270-767-30393	Sequence 30393, A
C 261	17	0.9	3021	4	US-09-556-877-182	Sequence 182, App	334	16	0.8	186	4	US-09-248-796A-13773	Sequence 9377, Ap
C 262	17	0.9	3021	4	US-09-620-412C-182	Sequence 182, App	335	16	0.8	192	4	US-09-762-960-5	Sequence 5, Appl1
C 263	17	0.9	3021	4	US-09-598-419-182	Sequence 182, App	336	16	0.8	192	4	US-09-248-796A-7100	Sequence 7100, Ap
C 264	17	0.9	3045	4	US-09-596-248D-24	Sequence 24, App	337	16	0.8	232	4	US-09-270-767-26013	Sequence 26013, A
C 265	17	0.9	3186	4	US-09-484-970B-168	Sequence 168, App	338	16	0.8	258	4	US-09-248-796A-13773	Sequence 13773, A
C 266	17	0.9	3200	4	US-09-596-248D-46	Sequence 46, App	339	16	0.8	261	4	US-09-248-796A-11344	Sequence 11344, Ap
C 267	17	0.9	3255	4	US-09-016-434-1471	Sequence 1471, Ap	340	16	0.8	270	4	US-09-513-999C-14881	Sequence 14881, A
C 268	17	0.9	3324	4	US-09-612-402B-24	Sequence 24, Appl	341	16	0.8	270	4	US-09-513-999C-14881	Sequence 14881, A
C 269	17	0.9	3331	3	US-08-864-038A-2	Sequence 2, Appl1	342	16	0.8	271	3	US-09-328-111-632	Sequence 632, App
C 270	17	0.9	3331	3	US-08-864-038A-4	Sequence 4, Appl1	343	16	0.8	273	3	US-09-248-796A-13017	Sequence 13017, A
C 271	17	0.9	3354	4	US-09-612-402B-23	Sequence 23, Appl1	344	16	0.8	283	3	US-09-172-711-25	Sequence 25, Appl
C 272	17	0.9	3388	1	US-08-197-792-32	Sequence 32, Appl	345	16	0.8	288	4	US-09-621-976-10038	Sequence 10038, A
C 273	17	0.9	3588	1	US-08-459-850-32	Sequence 32, Appl	346	16	0.8	292	4	US-09-621-976-10076	Sequence 10076, A
C 274	17	0.9	3588	1	US-08-459-214-32	Sequence 32, Appl	347	16	0.8	293	4	US-09-313-294A-958	Sequence 958, App
C 275	17	0.9	3660	4	US-09-517-467B-3	Sequence 3, Appl1	348	16	0.8	293	4	US-09-016-434-1032	Sequence 1032, Ap
C 276	17	0.9	3728	1	US-08-111-939-1	Sequence 1, Appl1	349	16	0.8	297	4	US-09-313-294A-945	Sequence 945, Ap
C 277	17	0.9	3747	1	US-08-044-618-5	Sequence 5, Appl1	350	16	0.8	303	4	US-09-248-796A-7417	Sequence 7417, Ap
C 278	17	0.9	3792	3	US-08-860-886-1	Sequence 1, Appl1	351	16	0.8	309	4	US-09-313-294A-4076	Sequence 4076, Ap
C 279	17	0.9	3852	4	US-09-245-248B-29	Sequence 29, Appl	352	16	0.8	309	4	US-09-513-999C-26869	Sequence 26869, A
C 280	17	0.9	3887	4	US-09-976-594-660	Sequence 660, App	353	16	0.8	309	4	US-09-513-999C-27757	Sequence 27757, A
C 281	17	0.9	3991	3	US-08-506-296B-3	Sequence 3, Appl1	354	16	0.8	311	4	US-09-313-294A-7021	Sequence 7021, Ap
C 282	17	0.9	4059	2	US-08-485-139-1	Sequence 1, Appl1	355	16	0.8	315	4	US-09-248-796A-12307	Sequence 12307, A
C 283	17	0.9	4059	3	US-08-750-357-1	Sequence 1, Appl1	356	16	0.8	320	4	US-09-270-767-29475	Sequence 29475, A
C 284	17	0.9	4133	4	US-09-688-188B-11	Sequence 11, Appl	357	16	0.8	322	4	US-09-621-976-1649	Sequence 1649, A
C 285	17	0.9	4133	4	US-09-291-417D-11	Sequence 11, Appl	358	16	0.8	328	4	US-09-270-767-8036	Sequence 8036, Ap
C 286	17	0.9	4218	1	US-09-081-385-8	Sequence 8, Appl1	359	16	0.8	328	4	US-09-270-767-8036	Sequence 8036, Ap
C 287	17	0.9	4418	4	US-09-976-594-773	Sequence 773, App	360	16	0.8	331	4	US-09-462-917A-51	Sequence 51, Appl
C 288	17	0.9	4432	4	US-09-774-528-148	Sequence 148, App	361	16	0.8	333	4	US-09-621-976-18183	Sequence 18183, A
C 289	17	0.9	4435	4	US-09-612-402B-1	Sequence 1, Appl1	362	16	0.8	336	4	US-09-248-796A-7944	Sequence 7944, Ap
C 290	17	0.9	4453	1	US-08-770-761A-4	Sequence 4, Appl1	363	16	0.8	339	4	US-09-621-976-1333	Sequence 1333, Ap
C 291	17	0.9	4540	1	US-08-770-761A-6	Sequence 6, Appl1	364	16	0.8	351	4	US-09-248-796A-10722	Sequence 10722, A
C 292	17	0.9	4621	1	US-08-770-761A-1	Sequence 1, Appl1	365	16	0.8	352	4	US-09-513-999C-11862	Sequence 11862, A
C 293	17	0.9	4824	2	US-08-485-139-5	Sequence 5, Appl1	366	16	0.8	360	4	US-10-101-464A-395	Sequence 395, App
C 294	17	0.9	4824	2	US-08-750-357-5	Sequence 5, Appl1	367	16	0.8	362	4	US-09-513-999C-3622	Sequence 3622, Ap
C 295	17	0.9	5257	4	US-09-917-254-47	Sequence 47, Appl1	368	16	0.8	363	4	US-09-621-976-18182	Sequence 18182, A
C 296	17	0.9	5962	1	US-08-188-582-10	Sequence 10, Appl	369	16	0.8	370	4	US-09-710-279-245	Sequence 245, App
C 297	17	0.9	5962	1	US-08-646-715-10	Sequence 10, Appl	370	16	0.8	370	4	US-09-270-767-8290	Sequence 8290, Ap
C 298	17	0.9	6223	4	US-09-620-312D-459	Sequence 459, App	371	16	0.8	370	4	US-09-270-767-8290	Sequence 8290, Ap
C 299	17	0.9	6304	4	US-09-620-312D-461	Sequence 461, App	372	16	0.8	370	4	US-09-270-767-8290	Sequence 8290, Ap
C 300	17	0.9	6382	4	US-09-620-312D-460	Sequence 460, App	373	16	0.8	373	4	US-09-710-279-3015	Sequence 3015, Ap
C 301	17	0.9	14736	4	US-08-961-527-171	Sequence 171, App	374	16	0.8	378	3	US-08-513-974B-33	Sequence 33, Appl
C 302	17	0.9	15936	4	US-09-147-119-1	Sequence 1, Appl1	375	16	0.8	378	3	US-08-776-971-28	Sequence 28, Appl
C 303	17	0.9	24979	2	US-08-147-777-3	Sequence 3, Appl1	376	16	0.8	378	4	US-09-461-436B-33	Sequence 33, Appl
C 304	17	0.9	24979	5	PCT-US93-03985-3	Sequence 3, Appl1	377	16	0.8	378	4	US-09-576-239B-28	Sequence 28, Appl
C 305	17	0.9	24979	5	PCT-US93-03985-3	Sequence 3, Appl1	378	16	0.8	381	4	US-09-270-767-7989	Sequence 7989, Ap
C 306	17	0.9	32155	4	US-08-311-731A-1	Sequence 1, Appl1	379	16	0.8	382	4	US-09-513-999C-11347	Sequence 11347, A
C 307	17	0.9	42235	3	US-09-199-637A-1	Sequence 1, Appl1	380	16	0.8	406	3	US-08-899-786-24	Sequence 24, Appl
C 308	17	0.9	44377	2	US-08-804-227C-7	Sequence 7, Appl1	381	16	0.8	412	4	US-09-513-999C-11346	Sequence 11346, A
C 309	17	0.9	44377	2	US-08-804-198-1	Sequence 1, Appl1	382	16	0.8	426	4	US-09-621-976-11124	Sequence 11724, A
C 310	17	0.9	48763	4	US-09-916-204-3	Sequence 3, Appl1	383	16	0.8	434	3	US-08-513-974B-165	Sequence 365, App
C 311	17	0.9	48763	4	US-10-282-048-3	Sequence 3, Appl1	384	16	0.8	434	3	US-08-776-971-105	Sequence 105, App
C 312	17	0.9	87350	4	US-08-781-891-79	Sequence 79, Appl	385	16	0.8	440	4	US-09-576-290-105	Sequence 105, App
C 313	17	0.9	87350	4	US-09-618-166-79	Sequence 79, Appl	386	16	0.8	440	4	US-09-270-767-1375	Sequence 1375, App
C 314	17	0.9	87543	4	US-09-791-211-3	Sequence 3, Appl1	387	16	0.8	444	4	US-09-270-767-16657	Sequence 16657, A
C 315	17	0.9	114793	4	US-10-148-806-3	Sequence 3, Appl1	388	16	0.8	444	4	US-09-621-976-962	Sequence 962, App
C 316	17	0.9	4403765	3	US-09-103-840A-2	Sequence 1, Appl1	389	16	0.8	444	4	US-09-248-796A-5986	Sequence 5986, App
C 317	17	0.9	441529	3	US-09-103-840A-1	Sequence 32, Appl	390	16	0.8	446	4	US-09-641-638-500	Sequence 500, App
C 318	16	0.8	20	4	US-09-596-248D-32	Sequence 33, Appl	391	16	0.8	446	4	US-10-170-097-500	Sequence 500, App
C 319	16	0.8	20	4	US-09-596-248D-33	Sequence 33, Appl	392	16	0.8	446	4	US-10-170-097-500	Sequence 500, App

C 393	16	0.8	447	4	US-09-621-976-17257	Sequence 17257, A	466	16	0.8	838	4	US-08-781-986A-827	Sequence 827, App
C 394	16	0.8	448	4	US-09-270-767-4398	Sequence 4398, App	467	16	0.8	842	3	US-08-952-796-1	Sequence 1, Appli
C 395	16	0.8	448	4	US-09-270-767-19680	Sequence 19680, A	468	16	0.8	842	3	US-08-940-136-759	Sequence 259, App
C 396	16	0.8	450	2	US-08-966-316-5	Sequence 5, Appli	C 469	16	0.8	855	4	US-09-248-796A-1869	Sequence 1869, App
C 397	16	0.8	456	4	US-09-513-909C-11345	Sequence 11345, A	C 470	16	0.8	857	4	US-09-270-767-28454	Sequence 28454, A
C 398	16	0.8	462	4	US-09-401-064-165	Sequence 165, App	C 471	16	0.8	857	4	US-09-919-039-248	Sequence 248, App
C 399	16	0.8	462	4	US-09-188-930-224	Sequence 224, App	C 472	16	0.8	858	4	US-09-482-273-46	Sequence 46, Appli
C 400	16	0.8	470	3	US-09-312-283C-224	Sequence 224, App	C 473	16	0.8	863	1	US-08-448-606-7	Sequence 7, Appli
C 401	16	0.8	472	4	US-09-621-976-18485	Sequence 18485, A	C 474	16	0.8	870	4	US-09-248-796A-4317	Sequence 4317, App
C 402	16	0.8	473	4	US-09-621-976-274	Sequence 274, App	C 475	16	0.8	873	4	US-09-023-655-83	Sequence 381, App
C 403	16	0.8	477	4	US-09-583-110-886	Sequence 886, App	C 476	16	0.8	873	4	US-09-248-796A-6838	Sequence 6838, App
C 404	16	0.8	481	4	US-09-644-907B-5	Sequence 5, Appli	C 477	16	0.8	879	4	US-08-513-999C-1806	Sequence 1806, App
C 405	16	0.8	485	4	US-09-686-583B-34	Sequence 34, Appli	C 478	16	0.8	900	1	US-08-480-481-6	Sequence 6, Appli
C 406	16	0.8	486	4	US-09-513-999C-11348	Sequence 11348, A	C 479	16	0.8	900	4	US-09-252-991A-1626	Sequence 1626, App
C 407	16	0.8	489	4	US-09-270-767-10584	Sequence 10584, A	C 480	16	0.8	921	4	US-09-107-532A-839	Sequence 839, App
C 408	16	0.8	496	4	US-09-621-976-1717	Sequence 1717, App	C 481	16	0.8	922	4	US-09-620-312D-1031	Sequence 1031, App
C 409	16	0.8	497	4	US-09-621-976-15691	Sequence 15691, A	C 482	16	0.8	924	3	US-08-983-409-3	Sequence 3, Appli
C 410	16	0.8	498	4	US-09-270-767-15691	Sequence 7392, App	C 483	16	0.8	924	3	US-09-107-532A-2518	Sequence 2518, App
C 411	16	0.8	498	4	US-09-270-767-22674	Sequence 22674, A	C 484	16	0.8	929	4	US-09-513-999C-14335	Sequence 14335, A
C 412	16	0.8	507	4	US-09-762-960-11	Sequence 11, Appli	C 485	16	0.8	935	4	US-09-919-039-26	Sequence 26, Appli
C 413	16	0.8	543	4	US-09-252-991A-11918	Sequence 11918, A	C 486	16	0.8	958	2	US-08-757-046A-5	Sequence 5, Appli
C 414	16	0.8	543	4	US-09-270-767-1945	Sequence 1945, App	C 487	16	0.8	958	3	US-09-447-208-5	Sequence 5, Appli
C 415	16	0.8	543	4	US-09-270-767-17227	Sequence 17227, A	C 488	16	0.8	958	3	US-09-135-988-5	Sequence 5, Appli
C 416	16	0.8	546	4	US-09-270-767-531	Sequence 531, App	C 489	16	0.8	958	3	US-09-277-716-5	Sequence 5, Appli
C 417	16	0.8	546	4	US-09-270-767-15813	Sequence 15813, A	C 490	16	0.8	958	3	US-08-597-274A-5	Sequence 5, Appli
C 418	16	0.8	546	4	US-09-799-451-89	Sequence 89, Appli	C 491	16	0.8	958	4	US-08-908-909-5	Sequence 5, Appli
C 419	16	0.8	550	4	US-09-686-583B-35	Sequence 35, Appli	C 492	16	0.8	958	4	US-09-609-161B-5	Sequence 5, Appli
C 420	16	0.8	561	4	US-09-248-796A-1741	Sequence 1741, App	C 493	16	0.8	958	4	US-08-990-103-5	Sequence 5, Appli
C 421	16	0.8	582	4	US-09-792-024-41	Sequence 41, Appli	C 494	16	0.8	958	4	US-09-746-485A-5	Sequence 5, Appli
C 422	16	0.8	603	3	US-08-952-786-14	Sequence 14, Appli	C 495	16	0.8	958	4	US-10-126-139-5	Sequence 5, Appli
C 423	16	0.8	606	4	US-09-621-976-16568	Sequence 16568, A	C 496	16	0.8	958	4	US-10-126-798-5	Sequence 5, Appli
C 424	16	0.8	609	1	US-07-834-902-2	Sequence 2, Appli	C 497	16	0.8	958	4	US-10-126-777-5	Sequence 5, Appli
C 425	16	0.8	609	1	US-08-018-994-2	Sequence 2, Appli	C 498	16	0.8	964	1	US-08-448-606-5	Sequence 5, Appli
C 426	16	0.8	609	1	US-08-294-675A-2	Sequence 2, Appli	C 499	16	0.8	966	4	US-09-489-039A-1797	Sequence 1797, App
C 427	16	0.8	609	5	PCT-US94-00928-1	Sequence 1, Appli	C 500	16	0.8	975	4	US-09-489-039A-632	Sequence 632, App
C 428	16	0.8	615	4	US-09-513-999C-730	Sequence 730, App	C 501	16	0.8	1000	4	US-09-023-655-1428	Sequence 1428, App
C 429	16	0.8	616	3	US-09-385-982-238	Sequence 238, App	C 502	16	0.8	1002	4	US-09-248-796A-5029	Sequence 5029, App
C 430	16	0.8	618	4	US-09-710-279-2183	Sequence 2183, App	C 503	16	0.8	1021	4	US-09-177-650-127	Sequence 127, App
C 431	16	0.8	618	4	US-09-799-451-148	Sequence 148, App	C 504	16	0.8	1044	4	US-09-710-279-6161	Sequence 461, App
C 432	16	0.8	633	4	US-09-248-796A-1367	Sequence 1367, App	C 505	16	0.8	1044	4	US-09-710-279-1267	Sequence 1267, App
C 433	16	0.8	633	4	US-09-248-796A-11732	Sequence 11732, A	C 506	16	0.8	1050	1	US-08-480-481-3	Sequence 3, Appli
C 434	16	0.8	640	4	US-09-270-767-1309	Sequence 1309, App	C 507	16	0.8	1050	1	US-08-480-481-4	Sequence 4, Appli
C 435	16	0.8	640	4	US-09-270-767-16591	Sequence 16591, A	C 508	16	0.8	1056	3	US-09-134-001C-2655	Sequence 2655, App
C 436	16	0.8	651	4	US-09-187-999-20	Sequence 20, Appli	C 509	16	0.8	1060	4	US-09-023-655-557	Sequence 357, App
C 437	16	0.8	657	4	US-09-248-796A-320	Sequence 320, App	C 510	16	0.8	1062	4	US-09-668-680-10	Sequence 10, Appli
C 438	16	0.8	662	3	US-08-927-219-42	Sequence 42, Appli	C 511	16	0.8	1113	3	US-09-172-353-1	Sequence 1, Appli
C 439	16	0.8	670	4	US-09-513-999C-14968	Sequence 14968, A	C 512	16	0.8	1123	4	US-09-976-594-411	Sequence 411, App
C 440	16	0.8	678	4	US-08-956-171E-792	Sequence 792, App	C 513	16	0.8	1123	3	US-08-983-409-5	Sequence 5, Appli
C 441	16	0.8	678	4	US-08-781-986A-792	Sequence 792, App	C 514	16	0.8	1133	3	US-09-248-796A-6764	Sequence 6764, App
C 442	16	0.8	689	4	US-09-513-999C-14965	Sequence 14965, A	C 515	16	0.8	1146	4	US-09-422-487-6	Sequence 6, Appli
C 443	16	0.8	690	4	US-09-248-796A-4601	Sequence 4601, App	C 516	16	0.8	1149	3	US-09-378-583B-4	Sequence 4, Appli
C 444	16	0.8	693	2	US-10-140-002-499	Sequence 499, App	C 517	16	0.8	1149	3	US-09-644-596B-128	Sequence 128, App
C 445	16	0.8	699	2	US-08-756-387B-7	Sequence 7, Appli	C 518	16	0.8	1149	3	US-09-644-596B-128	Sequence 128, App
C 446	16	0.8	699	3	US-09-285-873-7	Sequence 7, Appli	C 519	16	0.8	1152	2	US-08-933-750C-81	Sequence 81, Appli
C 447	16	0.8	699	4	US-09-944-277A-7	Sequence 7, Appli	C 520	16	0.8	1152	3	US-09-234-613-61	Sequence 61, Appli
C 448	16	0.8	707	3	US-08-998-416-729	Sequence 729, App	C 521	16	0.8	1155	4	US-09-248-796A-5987	Sequence 5987, App
C 449	16	0.8	707	3	US-08-998-416-940	Sequence 940, App	C 522	16	0.8	1155	4	US-09-248-796A-9481	Sequence 9481, App
C 450	16	0.8	711	3	US-09-134-001C-1248	Sequence 1248, App	C 523	16	0.8	1158	4	US-09-248-796A-4348	Sequence 4348, App
C 451	16	0.8	729	4	US-09-107-532A-120	Sequence 120, App	C 524	16	0.8	1161	4	US-09-686-583B-47	Sequence 47, Appli
C 452	16	0.8	742	4	US-09-513-999C-14957	Sequence 14957, A	C 525	16	0.8	1161	4	US-09-686-583B-49	Sequence 49, Appli
C 453	16	0.8	762	4	US-09-328-352-531	Sequence 531, App	C 526	16	0.8	1168	4	US-09-270-767-662	Sequence 662, App
C 454	16	0.8	773	4	US-08-897-956A-6	Sequence 6, Appli	C 527	16	0.8	1168	4	US-09-270-767-15944	Sequence 15944, A
C 455	16	0.8	774	2	US-08-756-387B-4	Sequence 4, Appli	C 528	16	0.8	1174	1	US-07-863-933-10	Sequence 10, Appli
C 456	16	0.8	774	3	US-08-756-387B-5	Sequence 5, Appli	C 529	16	0.8	1174	4	US-09-103-663-10	Sequence 10, Appli
C 457	16	0.8	774	3	US-09-285-873-4	Sequence 4, Appli	C 530	16	0.8	1174	3	US-09-270-767-27834	Sequence 27834, A
C 458	16	0.8	774	3	US-09-285-873-5	Sequence 5, Appli	C 531	16	0.8	1181	2	US-08-623-598-2	Sequence 2, Appli
C 459	16	0.8	774	4	US-09-944-277A-4	Sequence 4, Appli	C 532	16	0.8	1181	3	US-09-231-240-2	Sequence 2, Appli
C 460	16	0.8	774	4	US-09-944-277A-5	Sequence 5, Appli	C 533	16	0.8	1181	3	US-09-149-476-310	Sequence 310, App
C 461	16	0.8	801	1	US-07-959-946-4	Sequence 4, Appli	C 534	16	0.8	1191	3	US-09-046-992-3	Sequence 3, Appli
C 462	16	0.8	801	1	US-08-333-577-4	Sequence 4, Appli	C 535	16	0.8	1191	3	US-09-686-583B-45	Sequence 45, Appli
C 463	16	0.8	801	5	PCT-US92-08634-4	Sequence 4, Appli	C 536	16	0.8	1191	4	US-09-686-583B-46	Sequence 46, Appli
C 464	16	0.8	810	3	US-08-213-419B-12	Sequence 12, Appli	C 537	16	0.8	1198	2	US-08-756-387B-1	Sequence 1, Appli
C 465	16	0.8	838	4	US-08-956-171E-827	Sequence 827, App	C 538	16	0.8	1198	2	US-08-756-387B-3	Sequence 3, Appli

539	16	0.8	1198	3	US-09-285-873-1	Sequence 1, Appli	612	16	0.8	1860	4	US-09-270-767-1650	Sequence 12650, A
C 540	16	0.8	1198	3	US-09-285-873-3	Sequence 3, Appli	613	16	0.8	1881	4	US-09-556-916-13	Sequence 13, Appli
C 541	16	0.8	1198	4	US-09-944-277A-1	Sequence 1, Appli	614	16	0.8	1881	4	US-09-556-916-15	Sequence 15, Appli
C 542	16	0.8	1198	4	US-09-944-277A-3	Sequence 3, Appli	615	16	0.8	1881	4	US-09-556-916-19	Sequence 19, Appli
C 543	16	0.8	1203	3	US-09-086-010-1	Sequence 1, Appli	616	16	0.8	1881	4	US-09-556-916-21	Sequence 21, Appli
C 544	16	0.8	1212	4	US-09-149-476-186	Sequence 186, App	617	16	0.8	1884	4	US-09-556-916-1	Sequence 1, Appli
C 545	16	0.8	1212	4	US-09-710-279-1521	Sequence 1521, Ap	618	16	0.8	1884	4	US-09-556-916-3	Sequence 3, Appli
C 546	16	0.8	1218	4	US-09-336-536-22	Sequence 22, Appli	619	16	0.8	1884	4	US-09-556-916-7	Sequence 7, Appli
C 547	16	0.8	1239	4	US-09-248-796A-10434	Sequence 10434, A	620	16	0.8	1884	4	US-09-556-916-9	Sequence 9, Appli
C 548	16	0.8	1242	4	US-09-016-434-1283	Sequence 1283, Ap	621	16	0.8	1886	4	US-09-556-916-9	Sequence 9, Appli
C 549	16	0.8	1248	4	US-09-620-312D-936	Sequence 936, App	622	16	0.8	1894	4	US-09-252-991A-9847	Sequence 3847, Ap
C 550	16	0.8	1260	3	US-08-789-982-1	Sequence 1, Appli	C 622	16	0.8	1908	3	US-09-046-992-1	Sequence 1, Appli
C 551	16	0.8	1281	3	US-08-768-373-1	Sequence 1, Appli	623	16	0.8	1917	3	US-08-808-346-1	Sequence 1, Appli
C 552	16	0.8	1281	4	US-09-849-242A-1	Sequence 1, Appli	624	16	0.8	1926	1	US-07-901-703-12	Sequence 12, Appli
C 553	16	0.8	1285	4	US-09-370-767-14261	Sequence 1, Appli	625	16	0.8	1926	1	US-08-147-023-26	Sequence 26, Appli
C 554	16	0.8	1296	4	US-09-894-844-47	Sequence 14261, A	626	16	0.8	1926	1	US-08-278-728A-22	Sequence 22, Appli
C 555	16	0.8	1298	3	US-08-948-705-3	Sequence 47, Appli	627	16	0.8	1926	1	US-08-447-570-26	Sequence 26, Appli
C 556	16	0.8	1298	4	US-09-510-543-3	Sequence 3, Appli	628	16	0.8	1926	1	US-08-480-528A-9	Sequence 9, Appli
C 557	16	0.8	1317	4	US-09-248-796A-8424	Sequence 8424, Ap	629	16	0.8	1926	1	US-08-479-666-9	Sequence 9, Appli
C 558	16	0.8	1320	4	US-09-328-352-2477	Sequence 2477, Ap	630	16	0.8	1926	1	US-08-155-345A-22	Sequence 22, Appli
C 559	16	0.8	1344	4	US-09-016-434-1295	Sequence 1295, Ap	631	16	0.8	1926	1	US-08-406-672-22	Sequence 22, Appli
C 560	16	0.8	1356	1	US-07-978-892A-4	Sequence 4, Appli	632	16	0.8	1926	1	US-08-643-563A-22	Sequence 22, Appli
C 561	16	0.8	1365	4	US-09-800-729-36	Sequence 36, Appli	633	16	0.8	1926	1	US-08-447-570-26	Sequence 26, Appli
C 562	16	0.8	1440	1	US-07-978-892A-1	Sequence 1, Appli	634	16	0.8	1926	1	US-08-643-763A-22	Sequence 22, Appli
C 563	16	0.8	1456	4	US-09-976-594-779	Sequence 779, App	635	16	0.8	1926	1	US-08-462-623-22	Sequence 22, Appli
C 564	16	0.8	1463	4	US-09-325-932A-92	Sequence 92, App	636	16	0.8	1926	2	US-08-451-953A-22	Sequence 22, Appli
C 565	16	0.8	1463	4	US-09-270-767-8265	Sequence 92, Appli	637	16	0.8	1926	2	US-08-459-346-7	Sequence 7, Appli
C 566	16	0.8	1463	4	US-09-270-767-8265	Sequence 8265, Ap	638	16	0.8	1926	2	US-08-445-468A-22	Sequence 22, Appli
C 567	16	0.8	1479	2	US-08-199-485-1	Sequence 23547, A	639	16	0.8	1926	2	US-08-901-200A-9	Sequence 9, Appli
C 568	16	0.8	1482	4	US-09-252-991A-11453	Sequence 1, Appli	640	16	0.8	1926	2	US-08-449-700-26	Sequence 26, Appli
C 569	16	0.8	1505	1	US-07-915-246-1	Sequence 11453, A	641	16	0.8	1926	2	US-08-449-699A-26	Sequence 26, Appli
C 570	16	0.8	1505	4	US-09-620-312D-544	Sequence 1, Appli	642	16	0.8	1926	2	US-08-461-397A-22	Sequence 22, Appli
C 571	16	0.8	1506	4	US-09-016-434-1170	Sequence 544, App	643	16	0.8	1926	2	US-08-912-088-22	Sequence 22, Appli
C 572	16	0.8	1508	4	US-09-270-767-13489	Sequence 1170, Ap	644	16	0.8	1926	3	US-08-278-730A-22	Sequence 22, Appli
C 573	16	0.8	1509	4	US-09-134-000C-1868	Sequence 13489, A	645	16	0.8	1926	3	US-08-889-419-7	Sequence 7, Appli
C 574	16	0.8	1513	4	US-09-686-583B-39	Sequence 1868, Ap	646	16	0.8	1926	3	US-08-445-467-22	Sequence 22, Appli
C 575	16	0.8	1513	4	US-09-686-583B-41	Sequence 39, Appli	647	16	0.8	1926	3	US-08-480-515A-22	Sequence 22, Appli
C 576	16	0.8	1520	4	US-10-000-489-107	Sequence 41, Appli	648	16	0.8	1926	3	US-09-219-391-9	Sequence 9, Appli
C 577	16	0.8	1530	4	US-09-248-796A-2825	Sequence 107, App	649	16	0.8	1926	3	US-09-170-936-22	Sequence 22, Appli
C 578	16	0.8	1533	3	US-09-362-473-11	Sequence 2825, Ap	650	16	0.8	1926	3	US-08-402-542-7	Sequence 7, Appli
C 579	16	0.8	1536	4	US-09-270-767-12925	Sequence 11, Appli	651	16	0.8	1926	3	US-08-461-113-22	Sequence 22, Appli
C 580	16	0.8	1554	4	US-09-620-312D-802	Sequence 12925, A	652	16	0.8	1926	4	US-08-456-033-22	Sequence 22, Appli
C 581	16	0.8	1569	1	US-08-368-260-1	Sequence 802, App	653	16	0.8	1926	4	US-08-643-321-21	Sequence 21, Appli
C 582	16	0.8	1569	2	US-08-559-221-1	Sequence 1, Appli	654	16	0.8	1926	4	US-09-148-925C-26	Sequence 26, Appli
C 583	16	0.8	1581	4	US-09-252-991A-3616	Sequence 1, Appli	655	16	0.8	1926	5	US-08-957-425-26	Sequence 26, Appli
C 584	16	0.8	1581	6	5449756-10	Sequence 3616, Ap	656	16	0.8	1926	5	PCT-US92-01968-22	Sequence 22, Appli
C 585	16	0.8	1644	4	US-09-252-991A-3661	Sequence 3661, Ap	657	16	0.8	1926	5	PCT-US93-05446-12	Sequence 12, Appli
C 586	16	0.8	1644	4	US-09-270-767-1620	Sequence 1620, Ap	658	16	0.8	1926	5	PCT-US93-07189-7	Sequence 7, Appli
C 587	16	0.8	1644	4	US-09-270-767-16902	Sequence 16902, A	659	16	0.8	1926	5	PCT-US93-07190-22	Sequence 22, Appli
C 588	16	0.8	1645	2	US-08-461-812-1	Sequence 1, Appli	660	16	0.8	1926	5	PCT-US93-07231-22	Sequence 22, Appli
C 589	16	0.8	1645	4	US-09-371-705-1	Sequence 1, Appli	661	16	0.8	1926	5	PCT-US93-08742-22	Sequence 22, Appli
C 590	16	0.8	1651	3	US-09-362-473-1	Sequence 1, Appli	662	16	0.8	1926	5	PCT-US93-08808-22	Sequence 22, Appli
C 591	16	0.8	1690	3	US-08-860-519-11	Sequence 11, Appli	663	16	0.8	1926	5	PCT-US93-08865-22	Sequence 22, Appli
C 592	16	0.8	1690	3	US-09-112-096-27	Sequence 27, Appli	664	16	0.8	1926	5	PCT-US93-10520-9	Sequence 9, Appli
C 593	16	0.8	1705	4	US-09-227-595-23	Sequence 23, Appli	665	16	0.8	1929	5	US-07-841-646-26	Sequence 26, Appli
C 594	16	0.8	1705	4	US-08-595-590B-23	Sequence 23, Appli	666	16	0.8	1929	5	PCT-US91-07665-3	Sequence 3, Appli
C 595	16	0.8	1721	4	US-09-336-536-21	Sequence 23, Appli	667	16	0.8	1932	4	US-09-248-796A-11338	Sequence 11338, A
C 596	16	0.8	1725	4	US-09-634-238-130	Sequence 21, Appli	668	16	0.8	1935	4	US-09-778-510-21	Sequence 21, Appli
C 597	16	0.8	1743	4	US-09-556-916-17	Sequence 130, App	669	16	0.8	1939	4	US-09-636-215-817	Sequence 817, App
C 598	16	0.8	1743	4	US-09-556-916-23	Sequence 17, Appli	670	16	0.8	1959	4	US-09-685-168A-817	Sequence 817, App
C 599	16	0.8	1746	4	US-09-556-916-5	Sequence 5, Appli	671	16	0.8	1959	4	US-09-679-426-817	Sequence 817, App
C 600	16	0.8	1746	4	US-09-556-916-11	Sequence 11, Appli	672	16	0.8	1969	1	US-07-937-608-28	Sequence 28, Appli
C 601	16	0.8	1757	4	US-09-270-767-13876	Sequence 11, Appli	673	16	0.8	1969	4	US-08-029-170-28	Sequence 28, Appli
C 602	16	0.8	1787	4	US-09-398-522-109	Sequence 13876, A	674	16	0.8	2001	4	US-09-443-745-28	Sequence 28, Appli
C 603	16	0.8	1800	4	US-09-773-426A-14	Sequence 109, App	675	16	0.8	2015	1	US-09-248-796A-8777	Sequence 8777, Ap
C 604	16	0.8	1800	4	US-10-314-881-14	Sequence 14, Appli	676	16	0.8	2015	3	US-07-937-609-25	Sequence 25, Appli
C 605	16	0.8	1827	3	US-09-134-001C-1018	Sequence 1018, Ap	677	16	0.8	2015	3	US-08-029-1170-25	Sequence 25, Appli
C 606	16	0.8	1827	4	US-09-248-796A-5523	Sequence 1018, Ap	678	16	0.8	2022	4	US-09-443-745-25	Sequence 25, Appli
C 607	16	0.8	1832	4	US-09-686-583B-42	Sequence 9523, Ap	679	16	0.8	2034	4	US-09-270-767-11223	Sequence 12223, A
C 608	16	0.8	1832	4	US-09-686-583B-44	Sequence 42, Appli	680	16	0.8	2035	4	US-09-894-698-1	Sequence 1, Appli
C 609	16	0.8	1836	4	US-09-248-796A-10454	Sequence 44, Appli	681	16	0.8	2035	4	US-09-894-698-3	Sequence 3, Appli
C 610	16	0.8	1842	4	US-09-489-039A-2888	Sequence 10454, A	682	16	0.8	2051	1	US-08-343-785-7	Sequence 7, Appli
C 611	16	0.8	1842	4	US-09-248-796A-2421	Sequence 2888, Ap	683	16	0.8	2051	1	US-08-463-221-7	Sequence 7, Appli
						Sequence 2421, Ap	C 684	16	0.8	2051	3	US-08-946-458-7	Sequence 7, Appli

C 685	16	0.8	2070	4	US-09-107-532A-1284	Sequence 1284, Ap	758	16	0.8	3516	4	US-09-710-279-3852	Sequence 3852, Ap
C 686	16	0.8	2111	1	US-08-343-785-1	Sequence 1, Appli	C 759	16	0.8	3552	4	US-09-710-279-3752	Sequence 3752, Ap
C 687	16	0.8	2111	2	US-08-462-221-1	Sequence 1, Appli	C 760	16	0.8	3583	3	US-08-549-846-2	Sequence 2, Appli
C 688	16	0.8	2111	3	US-08-946-458-1	Sequence 1, Appli	C 761	16	0.8	3618	4	US-09-710-279-3564	Sequence 3564, Ap
C 689	16	0.8	2169	4	US-09-022-655-870	Sequence 870, App	C 762	16	0.8	3639	4	US-09-636-215-779	Sequence 779, App
C 690	16	0.8	2207	3	US-08-956-322-3	Sequence 3, Appli	C 763	16	0.8	3639	4	US-09-685-166A-779	Sequence 779, App
C 691	16	0.8	2225	4	US-09-484-970B-33	Sequence 33, Appli	C 764	16	0.8	3639	4	US-09-679-426-779	Sequence 779, App
C 692	16	0.8	2232	4	US-09-248-796A-3250	Sequence 3250, Ap	C 765	16	0.8	3804	4	US-09-620-312D-894	Sequence 894, App
C 693	16	0.8	2243	3	US-07-937-609-15	Sequence 15, Appli	C 766	16	0.8	3845	4	US-09-620-312D-554	Sequence 554, App
C 694	16	0.8	2243	3	US-08-029-170-15	Sequence 15, Appli	C 767	16	0.8	3876	4	US-09-849-602-4	Sequence 4, Appli
C 695	16	0.8	2243	4	US-09-443-745-15	Sequence 15, Appli	C 768	16	0.8	3892	4	US-09-665-189A-73	Sequence 73, Appli
C 696	16	0.8	2253	4	US-09-773-426A-8	Sequence 8, Appli	C 769	16	0.8	3895	4	US-09-730-279-4021	Sequence 4021, Ap
C 697	16	0.8	2253	4	US-10-314-881-8	Sequence 8, Appli	C 770	16	0.8	3923	2	US-08-199-485-2	Sequence 2, Appli
C 698	16	0.8	2261	4	US-09-774-528-128	Sequence 128, App	C 771	16	0.8	4065	4	US-09-016-434-1105	Sequence 1105, Ap
C 699	16	0.8	2266	4	US-09-495-823-8	Sequence 8, Appli	C 772	16	0.8	4078	4	US-09-016-434-1120	Sequence 1120, Ap
C 700	16	0.8	2277	4	US-09-248-796A-2537	Sequence 2537, Ap	C 773	16	0.8	4232	4	US-09-270-767-12086	Sequence 12086, A
C 701	16	0.8	2280	4	US-09-248-796A-5317	Sequence 5317, Ap	C 774	16	0.8	4453	3	US-09-453-702B-90	Sequence 90, Appli
C 702	16	0.8	2302	4	US-09-620-312D-915	Sequence 915, App	C 775	16	0.8	4458	4	US-09-811-469-1	Sequence 1, Appli
C 703	16	0.8	2306	6	5198359-3	Sequence 5198359	C 776	16	0.8	4458	4	US-10-370-659-1	Sequence 1, Appli
C 704	16	0.8	2306	6	5449756-3	Patent No. 5449756	C 777	16	0.8	4481	3	US-09-041-886-18	Sequence 18, Appli
C 705	16	0.8	2310	4	US-09-919-039-249	Sequence 249, App	C 778	16	0.8	4481	4	US-09-648-281-1	Sequence 1, Appli
C 706	16	0.8	2310	4	US-09-919-039-249	Sequence 249, App	C 779	16	0.8	4481	4	US-09-707-919A-20	Sequence 20, Appli
C 707	16	0.8	2329	3	US-08-956-322-1	Sequence 1, Appli	C 780	16	0.8	4481	4	US-09-083-268-2	Sequence 2, Appli
C 708	16	0.8	2352	4	US-09-533-029-117	Sequence 117, App	C 781	16	0.8	4512	4	US-09-792-616-2	Sequence 2, Appli
C 709	16	0.8	2352	4	US-09-724-586A-2	Sequence 2, Appli	C 782	16	0.8	4612	4	US-09-626-301-1	Sequence 1, Appli
C 710	16	0.8	2352	4	US-09-600-823-2	Sequence 2, Appli	C 783	16	0.8	4612	4	US-09-566-921-4	Sequence 4, Appli
C 711	16	0.8	2370	1	US-08-104-072B-7	Sequence 7, Appli	C 784	16	0.8	4642	4	US-09-626-301-3	Sequence 3, Appli
C 712	16	0.8	2370	1	US-08-351-413-8	Sequence 8, Appli	C 785	16	0.8	4739	3	US-08-685-871-1	Sequence 1, Appli
C 713	16	0.8	2370	2	US-09-025-583-8	Sequence 8, Appli	C 786	16	0.8	4853	3	US-08-881-450A-22	Sequence 22, Appli
C 714	16	0.8	2417	4	US-09-216-333B-306	Sequence 306, App	C 787	16	0.8	4890	4	US-09-677-046A-3	Sequence 3, Appli
C 715	16	0.8	2417	4	US-09-216-333B-308	Sequence 308, App	C 788	16	0.8	4933	4	US-09-677-046A-7	Sequence 7, Appli
C 716	16	0.8	2433	4	US-08-999-689A-2	Sequence 2, Appli	C 789	16	0.8	4970	4	US-09-816-095-1	Sequence 1, Appli
C 717	16	0.8	2433	4	US-09-944-807-3	Sequence 3, Appli	C 790	16	0.8	5000	4	US-08-956-171E-241	Sequence 241, App
C 718	16	0.8	2480	4	US-09-799-451-87	Sequence 87, Appli	C 791	16	0.8	5000	4	US-08-781-986A-241	Sequence 241, App
C 719	16	0.8	2493	4	US-09-252-991A-11987	Sequence 11987, A	C 792	16	0.8	5133	5	US-09-023-655-1290	Sequence 1290, Ap
C 720	16	0.8	2556	4	US-09-817-310-1	Sequence 1, Appli	C 793	16	0.8	5137	5	PCT-US96-01314-39	Sequence 39, Appli
C 721	16	0.8	2560	3	US-09-305-640-1	Sequence 1, Appli	C 794	16	0.8	5138	2	US-08-476-062A-39	Sequence 39, Appli
C 722	16	0.8	2565	4	US-09-105-058C-26	Sequence 26, Appli	C 795	16	0.8	5170	4	US-09-677-046A-5	Sequence 5, Appli
C 723	16	0.8	2571	4	US-09-248-796A-1986	Sequence 1986, App	C 796	16	0.8	5394	3	US-08-688-376-1	Sequence 1, Appli
C 724	16	0.8	2748	4	US-09-270-767-13675	Sequence 13675, A	C 797	16	0.8	5614	4	US-08-956-171E-99	Sequence 99, Appli
C 725	16	0.8	2797	4	US-09-799-451-563	Sequence 563, App	C 798	16	0.8	5614	4	US-08-781-986A-99	Sequence 99, Appli
C 726	16	0.8	2823	4	US-09-704-611-4	Sequence 4, Appli	C 799	16	0.8	5668	3	US-09-112-096-14	Sequence 14, Appli
C 727	16	0.8	2868	4	US-10-140-002-119	Sequence 119, App	C 800	16	0.8	5668	4	US-09-636-215-777	Sequence 777, App
C 728	16	0.8	2868	4	US-09-221-017B-863	Sequence 863, App	C 801	16	0.8	5668	4	US-09-685-166A-777	Sequence 777, App
C 729	16	0.8	2892	4	US-09-704-611-3	Sequence 3, Appli	C 802	16	0.8	5668	4	US-09-679-426-777	Sequence 777, App
C 730	16	0.8	2914	4	US-09-177-650-6	Sequence 6, Appli	C 803	16	0.8	5682	4	US-10-164-595-1	Sequence 1, Appli
C 731	16	0.8	2991	4	US-09-252-991A-12025	Sequence 12025, A	C 804	16	0.8	5926	4	US-09-917-254-41	Sequence 41, Appli
C 732	16	0.8	3014	1	US-08-629-939-1	Sequence 1, Appli	C 805	16	0.8	6203	3	US-09-114-218-3	Sequence 3, Appli
C 733	16	0.8	3014	1	US-08-759-873-1	Sequence 1, Appli	C 806	16	0.8	7060	4	US-09-221-017B-479	Sequence 479, App
C 734	16	0.8	3014	4	US-09-016-434-1244	Sequence 1244, Ap	C 807	16	0.8	7063	4	US-09-485-632B-5	Sequence 5, Appli
C 735	16	0.8	3105	3	US-08-542-635-1	Sequence 1, Appli	C 808	16	0.8	7445	3	US-09-178-973B-8	Sequence 8, Appli
C 736	16	0.8	3109	4	US-08-938-291A-1	Sequence 1, Appli	C 809	16	0.8	7445	3	US-09-419-568F-8	Sequence 8, Appli
C 737	16	0.8	3109	4	US-09-589-619-1	Sequence 1, Appli	C 810	16	0.8	7445	3	US-09-354-243B-8	Sequence 8, Appli
C 738	16	0.8	3153	4	US-09-710-279-3348	Sequence 3348, Ap	C 811	16	0.8	7481	4	US-08-956-171E-236	Sequence 236, App
C 739	16	0.8	3161	4	US-09-799-451-385	Sequence 385, App	C 812	16	0.8	7680	3	US-08-781-986A-236	Sequence 236, App
C 740	16	0.8	3209	4	US-09-976-594-671	Sequence 671, App	C 813	16	0.8	7680	3	US-09-210-748A-3	Sequence 3, Appli
C 741	16	0.8	3228	4	US-09-799-451-752	Sequence 752, App	C 814	16	0.8	7680	4	US-09-939-581A-3	Sequence 3, Appli
C 742	16	0.8	3245	4	US-09-774-528-352	Sequence 352, App	C 815	16	0.8	7812	4	US-09-485-632B-9	Sequence 9, Appli
C 743	16	0.8	3248	4	US-09-976-594-418	Sequence 418, App	C 816	16	0.8	8146	4	US-09-976-594-725	Sequence 725, App
C 744	16	0.8	3251	3	US-09-085-199B-6	Sequence 6, Appli	C 817	16	0.8	8146	4	US-09-976-594-725	Sequence 725, App
C 745	16	0.8	3263	3	US-09-710-279-3595	Sequence 3595, Ap	C 818	16	0.8	9416	4	US-08-823-895A-26	Sequence 26, Appli
C 746	16	0.8	3267	4	US-09-710-279-4042	Sequence 4042, Ap	C 819	16	0.8	9416	4	US-10-104-966-13	Sequence 13, Appli
C 747	16	0.8	3273	4	US-09-270-767-10465	Sequence 10465, A	C 820	16	0.8	9599	3	US-09-014-416-2	Sequence 2, Appli
C 748	16	0.8	3282	4	US-09-976-594-708	Sequence 708, App	C 821	16	0.8	10014	3	US-08-927-219-130	Sequence 130, App
C 749	16	0.8	3282	4	US-09-919-039-274	Sequence 274, App	C 822	16	0.8	10034	3	US-09-771-357-102	Sequence 102, App
C 750	16	0.8	3332	4	US-09-710-279-3928	Sequence 3928, App	C 823	16	0.8	10660	2	US-08-267-803B-8	Sequence 8, Appli
C 751	16	0.8	3350	3	US-09-110-116-2	Sequence 2, Appli	C 824	16	0.8	10660	3	US-09-041-886-16	Sequence 16, Appli
C 752	16	0.8	3350	3	US-08-405-392-1	Sequence 1, Appli	C 825	16	0.8	11531	1	US-08-068-942A-1	Sequence 1, Appli
C 753	16	0.8	3385	3	US-08-487-691-1	Sequence 1, Appli	C 826	16	0.8	11531	1	US-08-442-806-1	Sequence 1, Appli
C 754	16	0.8	3385	3	US-08-666-221B-3	Sequence 3, Appli	C 827	16	0.8	11531	1	US-09-355-295B-1	Sequence 1, Appli
C 755	16	0.8	3385	4	US-08-666-221B-9	Sequence 9, Appli	C 828	16	0.8	11558	5	PCT-US93-06211-23	Sequence 23, Appli
C 756	16	0.8	3385	4	US-08-189-738A-1	Sequence 1, Appli	C 829	16	0.8	11613	3	US-09-453-702B-42	Sequence 42, Appli
C 757	16	0.8	3465	3	US-08-914-999-5	Sequence 5, Appli	C 830	16	0.8	11917	4	US-09-566-921-32	Sequence 32, Appli

C 831	16	0.8	11917	4	US-09-566-921-32	Sequence 32, Appl	C 904	15	0.8	54	2	US-08-541-780-44	Sequence 44, Appl
C 832	16	0.8	12732	4	US-09-060-756-1	Sequence 1, Appl1	C 905	15	0.8	60	3	US-08-911-894-49	Sequence 49, Appl
C 833	16	0.8	12732	4	US-09-670-314-1	Sequence 1, Appl1	C 906	15	0.8	63	6	5498600-29	Patent No. 5498600
C 834	16	0.8	13542	4	US-08-956-171E-154	Sequence 154, App	C 907	15	0.8	80	1	US-08-425-336-119	Sequence 119, App
C 835	16	0.8	13542	4	US-08-781-986A-154	Sequence 154, App	C 908	15	0.8	80	1	US-08-488-113B-119	Sequence 119, App
C 836	16	0.8	13842	3	US-09-105-537-30	Sequence 30, Appl	C 909	15	0.8	80	1	US-08-488-113B-119	Sequence 119, App
C 837	16	0.8	13865	3	US-09-009-217-11	Sequence 11, Appl	C 910	15	0.8	80	1	US-08-477-484B-119	Sequence 119, App
C 838	16	0.8	13865	3	US-09-009-656-11	Sequence 11, Appl	C 911	15	0.8	80	1	US-08-477-484B-119	Sequence 119, App
C 839	16	0.8	13865	3	US-09-054-272-11	Sequence 11, Appl	C 912	15	0.8	80	1	US-08-107-669D-11	Sequence 11, App
C 840	16	0.8	15872	3	US-09-105-537-1	Sequence 1, Appl1	C 913	15	0.8	80	1	US-08-107-669D-11	Sequence 11, App
C 841	16	0.8	15872	3	US-09-091-609-3	Sequence 1, Appl1	C 914	15	0.8	80	1	US-08-472-788A-31	Sequence 31, Appl
C 842	16	0.8	15872	3	US-09-091-609-3	Sequence 1, Appl1	C 915	15	0.8	80	1	US-08-472-788A-31	Sequence 31, Appl
C 843	16	0.8	18853	4	US-09-820-005-3	Sequence 3, Appl1	C 916	15	0.8	80	1	US-08-472-788A-31	Sequence 31, Appl
C 844	16	0.8	18853	4	US-10-109-885-3	Sequence 3, Appl1	C 917	15	0.8	80	1	US-08-472-788A-31	Sequence 31, Appl
C 845	16	0.8	18853	4	US-08-961-527-86	Sequence 86, Appl	C 918	15	0.8	80	1	US-08-477-531B-62	Sequence 62, Appl
C 846	16	0.8	19390	4	US-08-961-527-86	Sequence 86, Appl	C 919	15	0.8	80	1	US-08-477-531B-62	Sequence 62, Appl
C 847	16	0.8	19718	3	US-08-961-527-99	Sequence 99, Appl	C 920	15	0.8	80	1	US-08-646-360-119	Sequence 62, Appl
C 848	16	0.8	22067	3	US-09-820-001-3	Sequence 99, Appl	C 921	15	0.8	80	1	US-08-646-360-119	Sequence 62, Appl
C 849	16	0.8	31960	3	US-09-841-158-5	Sequence 5, Appl1	C 922	15	0.8	80	2	US-08-646-360-119	Sequence 62, Appl
C 850	16	0.8	36741	3	US-09-301-665-3	Sequence 11, Appl	C 923	15	0.8	80	2	US-08-646-360-119	Sequence 62, Appl
C 851	16	0.8	36741	3	US-09-105-537-5	Sequence 3, Appl1	C 924	15	0.8	80	2	US-08-646-360-119	Sequence 62, Appl
C 852	16	0.8	38506	3	US-09-320-878-19	Sequence 5, Appl1	C 925	15	0.8	80	3	US-08-839-765-119	Sequence 62, Appl
C 853	16	0.8	38506	4	US-09-141-908-1	Sequence 5, Appl1	C 926	15	0.8	80	3	US-08-839-765-119	Sequence 62, Appl
C 854	16	0.8	38506	4	US-09-657-440-19	Sequence 19, Appl	C 927	15	0.8	80	3	US-08-839-765-119	Sequence 62, Appl
C 855	16	0.8	43095	4	US-09-676-519-17	Sequence 19, Appl	C 928	15	0.8	80	3	US-08-839-765-119	Sequence 62, Appl
C 856	16	0.8	43280	2	US-09-804-227C-1	Sequence 17, Appl	C 929	15	0.8	80	3	US-08-839-765-119	Sequence 62, Appl
C 857	16	0.8	50000	3	US-09-146-053-3	Sequence 1, Appl1	C 930	15	0.8	80	4	US-09-711-485-119	Sequence 119, App
C 858	16	0.8	51259	3	US-08-781-891-209	Sequence 3, Appl1	C 931	15	0.8	80	4	US-09-711-485-119	Sequence 119, App
C 859	16	0.8	51259	3	US-09-618-166-209	Sequence 209, App	C 932	15	0.8	80	4	US-09-711-485-119	Sequence 119, App
C 860	16	0.8	80200	4	US-09-851-896-3	Sequence 3, Appl1	C 933	15	0.8	80	4	US-09-711-485-119	Sequence 119, App
C 861	16	0.8	80246	4	US-09-078-294-4	Sequence 4, Appl1	C 934	15	0.8	80	4	US-09-270-767-4064	Sequence 141, App
C 862	16	0.8	80595	3	US-09-078-294-4	Sequence 3, Appl1	C 935	15	0.8	81	1	US-09-270-767-4064	Sequence 141, App
C 863	16	0.8	83450	4	US-09-811-469-3	Sequence 3, Appl1	C 936	15	0.8	81	2	US-08-447-169A-143	Sequence 143, App
C 864	16	0.8	83450	4	US-10-370-659-3	Sequence 3, Appl1	C 937	15	0.8	81	2	US-08-233-012C-143	Sequence 143, App
C 865	16	0.8	87563	3	US-09-453-702B-57	Sequence 57, Appl	C 938	15	0.8	90	4	US-09-860-474-143	Sequence 143, App
C 866	16	0.8	89916	4	US-09-816-095-3	Sequence 3, Appl1	C 939	15	0.8	93	3	US-09-331-793-12	Sequence 143, App
C 867	16	0.8	107820	4	US-09-792-616-1	Sequence 1, Appl1	C 940	15	0.8	94	4	US-08-976-413A-408	Sequence 143, App
C 868	16	0.8	116592	4	US-09-818-512-3	Sequence 3, Appl1	C 941	15	0.8	94	4	US-09-513-999C-29269	Sequence 143, App
C 869	16	0.8	128779	4	US-09-497-855A-38	Sequence 38, Appl1	C 942	15	0.8	99	4	US-09-270-767-4064	Sequence 143, App
C 870	16	0.8	148567	4	US-10-254-869-3	Sequence 3, Appl1	C 943	15	0.8	101	4	US-09-877-243A-153	Sequence 153, App
C 871	16	0.8	148567	4	US-09-801-876B-3	Sequence 3, Appl1	C 944	15	0.8	101	4	US-09-513-999C-19621	Sequence 153, App
C 872	16	0.8	193303	4	US-09-497-855A-37	Sequence 37, Appl	C 945	15	0.8	117	3	US-09-513-999C-21164	Sequence 153, App
C 873	16	0.8	193303	4	US-09-497-855A-44	Sequence 44, Appl	C 946	15	0.8	127	3	US-08-857-046A-28	Sequence 153, App
C 874	16	0.8	202001	4	US-09-734-674-3	Sequence 3, Appl1	C 947	15	0.8	157	4	US-09-621-976-7817	Sequence 28, Appl
C 875	16	0.8	229354	4	US-09-765-400-64	Sequence 3, Appl1	C 948	15	0.8	158	4	US-09-513-999C-11009	Sequence 11009, App
C 876	16	0.8	229354	4	US-09-705-400-64	Sequence 64, Appl	C 949	15	0.8	176	4	US-09-270-767-2963	Sequence 2963, App
C 877	16	0.8	320000	4	US-10-027-983-11	Sequence 11, Appl	C 950	15	0.8	176	4	US-09-270-767-2963	Sequence 2963, App
C 878	16	0.8	320000	4	US-09-198-452A-1	Sequence 1, Appl1	C 951	15	0.8	180	4	US-09-331-793-19	Sequence 180, App
C 879	16	0.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl1	C 952	15	0.8	186	4	US-09-248-796A-7468	Sequence 7468, App
C 880	16	0.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl1	C 953	15	0.8	186	4	US-09-513-999C-18069	Sequence 18069, App
C 881	16	0.8	1664976	4	US-09-692-570-1	Sequence 1, Appl1	C 954	15	0.8	189	4	US-09-248-796A-7901	Sequence 7901, App
C 882	16	0.8	1664976	4	US-09-692-570-1	Sequence 1, Appl1	C 955	15	0.8	190	3	US-09-513-999C-2444	Sequence 2444, App
C 883	15	0.8	18	3	US-09-289-466-52	Sequence 52, Appl	C 956	15	0.8	190	3	US-09-723-473-1	Sequence 473, App
C 884	15	0.8	18	4	US-09-478-189-28	Sequence 28, Appl	C 957	15	0.8	190	3	US-09-723-473-1	Sequence 473, App
C 885	15	0.8	20	4	US-09-422-978-4425	Sequence 425, App	C 958	15	0.8	190	3	US-09-723-473-1	Sequence 473, App
C 886	15	0.8	20	4	US-09-909-595-23	Sequence 23, Appl	C 959	15	0.8	192	4	US-09-723-520-1	Sequence 520, App
C 887	15	0.8	25	2	US-08-497-997C-13	Sequence 13, Appl	C 960	15	0.8	192	4	US-09-248-796A-8239	Sequence 8239, App
C 888	15	0.8	27	3	US-09-036-579-11	Sequence 11, Appl	C 961	15	0.8	195	4	US-09-248-796A-10135	Sequence 10135, App
C 889	15	0.8	27	3	US-09-550-374-11	Sequence 11, Appl	C 962	15	0.8	195	4	US-09-248-796A-9579	Sequence 9579, App
C 890	15	0.8	27	3	US-09-943-906-11	Sequence 11, Appl	C 963	15	0.8	199	4	US-09-513-999C-11157	Sequence 11157, App
C 891	15	0.8	27	3	US-09-397-885-13	Sequence 13, Appl	C 964	15	0.8	200	4	US-09-060-299-36	Sequence 36, Appl
C 892	15	0.8	35	3	US-09-969-362-13	Sequence 13, Appl	C 965	15	0.8	204	4	US-09-402-923A-36	Sequence 36, Appl
C 893	15	0.8	35	4	US-09-969-362-13	Sequence 13, Appl	C 966	15	0.8	205	4	US-09-252-991A-11819	Sequence 11819, App
C 894	15	0.8	36	1	US-07-960-510-12	Sequence 12, Appl	C 967	15	0.8	206	4	US-09-016-434-570	Sequence 570, App
C 895	15	0.8	36	1	US-07-960-510-12	Sequence 12, Appl	C 968	15	0.8	206	4	US-09-016-434-570	Sequence 570, App
C 896	15	0.8	36	1	US-08-863-639A-31	Sequence 31, Appl	C 969	15	0.8	210	2	US-08-487-031-16	Sequence 31, Appl
C 897	15	0.8	37	2	US-08-863-639A-31	Sequence 31, Appl	C 970	15	0.8	210	3	US-08-487-031-16	Sequence 31, Appl
C 898	15	0.8	37	2	US-08-863-639A-31	Sequence 31, Appl	C 971	15	0.8	210	3	US-08-487-031-16	Sequence 31, Appl
C 899	15	0.8	38	3	US-08-292-620A-2282	Sequence 2282, App	C 972	15	0.8	210	4	US-09-489-039A-6266	Sequence 6266, App
C 900	15	0.8	38	3	US-08-292-620A-2282	Sequence 2282, App	C 973	15	0.8	211	4	US-09-248-796A-12394	Sequence 12394, App
C 901	15	0.8	44	3	US-09-071-845-2282	Sequence 11, Appl	C 974	15	0.8	211	4	US-09-702-705-252	Sequence 252, App
C 902	15	0.8	50	2	US-08-190-199A-4	Sequence 4, Appl1	C 975	15	0.8	211	4	US-09-702-705-252	Sequence 252, App
C 903	15	0.8	54	1	US-07-731-157A-44	Sequence 44, Appl	C 976	15	0.8	211	4	US-09-614-124B-252	Sequence 252, App
												US-09-589-184-252	Sequence 252, App

977 15 0.8 211 4 US-09-658-824-252 Sequence 252, App
978 15 0.8 213 4 US-09-107-532A-3519 Sequence 3519, Ap
979 15 0.8 213 4 US-09-107-532A-3520 Sequence 3520, Ap
980 15 0.8 213 4 US-09-513-999C-3200 Sequence 3200, Ap
981 15 0.8 219 3 US-09-061-026-15 Sequence 15, Appl
982 15 0.8 219 3 US-09-061-026-19 Sequence 19, Appl
983 15 0.8 219 3 US-09-466-138-15 Sequence 15, Appl
984 15 0.8 219 3 US-09-466-138-19 Sequence 19, Appl
985 15 0.8 221 4 US-09-513-999C-9989 Sequence 9989, Ap
986 15 0.8 221 4 US-09-513-999C-12262 Sequence 12262, A
987 15 0.8 224 3 US-09-385-982-97 Sequence 97, Appl
988 15 0.8 225 4 US-09-513-999C-13673 Sequence 13673, A
989 15 0.8 226 4 US-09-513-999C-16872 Sequence 16872, A
990 15 0.8 233 4 US-09-445-803-4 Sequence 4, Appl1
991 15 0.8 234 4 US-09-489-039A-5121 Sequence 5121, Ap
992 15 0.8 234 4 US-09-248-796A-7364 Sequence 7364, Ap
993 15 0.8 235 4 US-09-621-976-13593 Sequence 13593, A
994 15 0.8 241 4 US-09-389-681-334 Sequence 334, App
995 15 0.8 241 4 US-09-620-405B-334 Sequence 334, App
996 15 0.8 241 4 US-09-433-826B-334 Sequence 334, App
997 15 0.8 241 4 US-09-604-287A-334 Sequence 334, App
998 15 0.8 241 4 US-09-834-759-334 Sequence 334, App
999 15 0.8 241 4 US-09-590-751A-334 Sequence 334, App
c1000 15 0.8 243 4 US-09-252-991A-4273 Sequence 4273, Ap

ALIGNMENTS

RESULT 1
US-08-306-691B-22
; Sequence 22, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039E
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-306-691B-22

Query Match 1.2%; Score 23; DB 1; Length 4626;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1240 AAGGTGCTGATTTGGCTTGC 1262
|||||
DB 3903 AAGGTGCTGATTTGGCTTGC 3925

RESULT 2

PCT-US93-06251-27
; Sequence 27, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Mickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SCULLY, SCOTT, MORPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US93-06251-27
Query Match 1.2%; Score 23; DB 5; Length 4626;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1240 AAGGTGCTGATTTGGCTTGC 1262
|||||
DB 3903 AAGGTGCTGATTTGGCTTGC 3925

RESULT 3
US-09-800-729-55
; Sequence 55, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709

PRIOR FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 217
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 55
 LENGTH: 609
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (554)
 OTHER INFORMATION: n equals a,t,g, or c
 US-09-800-729-55

Query Match 1.0%; Score 20; DB 4; Length 609;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 CACCTCTCCACCTCCACC 686
 Db 269 CACCTCTCCACCTCCACC 288

RESULT 4
 US-09-252-991A-1274
 Sequence 1274, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 1274
 LENGTH: 852
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1274

Query Match 1.0%; Score 20; DB 4; Length 852;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGCAGCAGCATTTGCTTAAC 1486
 Db 56 GGCAGCAGCATTTGCTTAAC 75

RESULT 5
 US-09-252-991A-1381/c
 Sequence 1381, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 1381
 LENGTH: 909
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1381

Query Match 1.0%; Score 20; DB 4; Length 909;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGCAGCAGCATTTGCTTAAC 1486
 Db 112 GGCAGCAGCATTTGCTTAAC 93

RESULT 6
 US-09-252-991A-1287/c
 Sequence 1287, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 1287
 LENGTH: 1092
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1287

Query Match 1.0%; Score 20; DB 4; Length 1092;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGCAGCAGCATTTGCTTAAC 1486
 Db 126 GGCAGCAGCATTTGCTTAAC 107

RESULT 7
 US-09-248-796A-4378
 Sequence 4378, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 PRIOR FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 4378
 LENGTH: 1680
 TYPE: DNA
 ORGANISM: Candida albicans
 US-09-248-796A-4378

Query Match 1.0%; Score 20; DB 4; Length 1680;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 TTGCTATTTGCTCTTGGT 1263
 Db 866 TTGCTATTTGCTCTTGGT 885

RESULT 8
US-09-248-796A-1640
; Sequence 1640, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1640
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1640

Query Match
Best Local Similarity 1.0%; Score 20; DB 4; Length 2838;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 CCTCTCCACCTCCACCACC 689
DB 1114 CCTCTCCACCTCCACCACC 1133

RESULT 9
US-09-228-986-11
; Sequence 11, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-11

Query Match
Best Local Similarity 1.0%; Score 20; DB 3; Length 3097;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 GTTGCTTTGGAGCTCAT 1406
DB 2556 GTTGCTTTGGAGCTCAT 2575

RESULT 10
US-10-101-464A-11
; Sequence 11, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-11

Query Match
Best Local Similarity 1.0%; Score 20; DB 4; Length 3097;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 GTTGCTTTGGAGCTCAT 1406
DB 2556 GTTGCTTTGGAGCTCAT 2575

RESULT 11
US-09-800-729-18
; Sequence 18, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044p1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 5720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-18

Query Match
Best Local Similarity 1.0%; Score 20; DB 4; Length 5720;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 CAACCTCCTCCACCTCCACC 686
DB 5431 CAACCTCCTCCACCTCCACC 5450

RESULT 12
US-09-755-665-46/c
; Sequence 46, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhir Das K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 46
LENGTH: 41100
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: GENOMIC DNA
US-09-755-665-46

Query Match
Best Local Similarity 1.0%; Score 20; DB 4; Length 41100;
Pred. No. 9.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 TGGGAGTGTCTCGGAGAGA 940
DB 22048 TGGGAGTGTCTCGGAGAGA 22029

RESULT 13

US-08-991-789A-168
Sequence 168, Application US/08991789A
Patent No. 6225054
GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 168:
US-08-991-789A-168

Query Match
Best Local Similarity 1.0%; Score 19; DB 3; Length 358;
Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 950 AGGCAGAGTTGAGATCAT 968
DB 228 AGGCAGAGTTGAGATCAT 246

RESULT 14
US-09-062-451-168

Sequence 168, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-062-451-168

Query Match
Best Local Similarity 1.0%; Score 19; DB 3; Length 358;
Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 950 AGGCAGAGTTGAGATCAT 968
DB 228 AGGCAGAGTTGAGATCAT 246

RESULT 15
US-09-598-326-168
Sequence 168, Application US/09598326
Patent No. 6423496
GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 247
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

US-09-598-326-168

Query Match
Best Local Similarity 1.0%; Score 19; DB 3; Length 358;
Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 950 AGGCAGAGTTGAGATCAT 968
DB 228 AGGCAGAGTTGAGATCAT 246

RESULT 15
US-09-598-326-168

APPLICATION NUMBER: US/09/598,326
 FILING DATE: 20-Jun-2000
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Potter, Jane E.R.
 REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 210121.419D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 168:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 168:
 US-09-598-326-168

Query Match 1.0%; Score 19; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred.No.28;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 950 AGGCAAGGTTGAGATCAT 968
 |||||
 DB 228 AGGCAAGGTTGAGATCAT 246

Search completed: November 13, 2004, 15:32:42
 Job time : 150 secs

Query Match 100.0%; Score 1944; DB 6; Length 1944;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTCTGGGCGCGCTCTCCGGGAGACTGGTGGCTCCATCTCCACCATCAAACTGCACA 60
Db 1 ATGTCTCGGCGCGCTCTCCGGGAGACTGGTGGCTCCATCTCCACCATCAAACTGCACA 60
QY 61 ACCAGCACTCTCTCCAGCTTCGGCTCCCTCCGCCACGACCTTCTCTCTCCGGCG 120
Db 61 ACCAGCACTCTCTCCAGCTTCGGCTCCCTCCGCCACGACCTTCTCTCTCCGGCG 120
QY 121 CCATCCATATTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 121 CCATCCATATTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 CCATCTCCACCACTCATCTTAAGCGGGGATCTCCACCTCTCTCTCTCTCTCTCTCTCA 240
Db 181 CCATCTCCACCACTCATCTTAAGCGGGGATCTCCACCTCTCTCTCTCTCTCTCTCTCA 240
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 REFERENCE 1
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 Increasing plant seed production
 Patent: WO 03072763-A 3 04-SEP-2003;
 Goring, Daphne (CA); Silva, Nancy (CA); Haffani, Yosr, Z. (CA)
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 1 Goring, D., Silva, N. and Haffani, Y. Z.
 Increasing plant seed production.
 Patent: WO 03072763-A 36 04-SEP-2003;
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 1 (bases 1 to 2098)
 REFERENCE
 Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M.,
 Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
 Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
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 Sakano,H., Sekurai,T., Satou,M., Seki,M., Shim,P., Yamada,K.,
 Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
 Direct Submission
 Submitted (01-JUL-2002) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT
 e-mail for correspondence: arabseq@stanford.edu
 The RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
 Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sekurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.
 The Salk, Stanford, PGSC (SSP) Consortium members constructed and
 sequenced the pUN1 (ORF) clones using the RAFL cDNAs: Tripp,M.,
 Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M.,
 Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R.,
 Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H.,
 Shim,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
 Tripp,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally
 to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
 (SSP/Stanford) contributed equally to this work as PIs.
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Query Match 70.4%; Score 1369.4; DB 8; Length 2188;
 Best Local Similarity 83.4%; Prid. No. 3.1e-269;
 Matches 1611; Conservative 0; Mismatches 291; Indels 30; Gaps 4;

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 Db 131 CTTCTCCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 190
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 Db 191 CTTCT 250
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 Db 251 A-----CT 298
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RESULT 9
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ORIGIN

Query Match 70.4%; Score 1367.8; DB 8; Length 1959;
Best Local Similarity 83.3%; Pired. No. 6,6e-269;
Matches 1610; Conservative 0; Mismatches 292; Indels 30; Gaps 4;

31 TCGCTTCATCTCCACATCAAACTCCACAAACCAACCACTCTCTCCAGCTTCGGCTCT 90
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VERSION BT008409.1 GI:30725491
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ACCESSION	AY089024
VERSION	AY089024.1 GI:21407798
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ORGANISM	Arabidopsis thaliana
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REFERENCE	
AUTHORS	Haas,B.U., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE	Full-length messenger RNA sequences greatly improve genome

annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE
22088475
PubMed
12093376
REFERENCE
2 (bases 1 to 2324)
Broyer, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
Full-length cDNA from Arabidopsis thaliana
TITLE
JOURNAL
Unpublished
3 (bases 1 to 2324)
Broyer, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
Direct Submission
TITLE
JOURNAL
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and GenBank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES
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ORIGIN

Query Match 69.0%; Score 1341.2; DB 8; Length 2324;
Best Local Similarity 82.8%; Pred. No. 1.8e-263;
Matches 1598; Conservative 0; Mismatches 363; Indels 28; Gaps 5;

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LOCUS	AX825736				
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ACCESSION	AX825736			linear	PAT 11-DEC-2003
VERSION	AX825736.1				
KEYWORDS	GI:39751253				
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ORGANISM	Zea mays Zea mays				

REFERENCE	Goring, D., Silva, N. and Haffani, Y. Z.
AUTHORS	Increasing plant seed production
TITLE	Patent: WO 03072763-A 34 04-SEP-2003;
JOURNAL	Goring, Daphne (CA) ; Silva, Nancy (CA)
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QY	853	GGGTTCCGTTAAGTCGACAAAGGTGTGTTGCCATGAGGGAAGAAGTGTCTGTAAAGAG	912
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DEFINITION Sequence 35 from Patent WO03072763.
ACCESSION AX825737
VERSION AX825737.1 GI:39751254
KEYWORDS
SOURCE
ORGANISM Glycine max (soybean)
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          Glycine.
REFERENCE 1
AUTHORS Goring, D., Silva, N. and Hafani, Y. Z.
TITLE Increasing plant seed production
JOURNAL Patent: WO 0307263-A 35 04-SEP-2003;
          Goring, Daphne (CA); Silva, Nancy (CA); Hafani, Yost, Z. (CA)
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Matches 848; Conservative 0; Mismatches 330; Indels 15; Gaps 3;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 06:51:43 ; Search time 649 Seconds

Title: US-10-069-304-1
Perfect score: 1944

Scoring table: IDENTITY_NUC

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	1341.2	69.0	2324	3	AAc36698	AAc36698 Arabidops
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7	605	31.1	1488	10	ACF36556	AtF36556 G. max
8	566.6	29.1	1812	10	ACF36554	AcF36554 O. sativa
9	329.2	16.9	685	10	ADK53814	Plant DNN
10	215.8	11.1	1703	3	AAc46629	Zea mays
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12	204.6	10.5	1419	3	ABE13121	Arabidops
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14	201	10.3	1950	6	ABE12861	Arabidops
15	199	10.2	1353	3	AAc42860	Arabidops
16	199	10.2	1353	6	ABE14106	Arabidops
17	199	10.2	1626	3	AAc48313	Arabidops
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ALIGNMENTS

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XX	Brassica napus PERK1 DNA.	
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XX	WO200114563-A1.	
XX	01-MAR-2001.	
XX	18-AUG-2000; 2000MC-CA000966.	
XX	19-AUG-1999; 99US-0149466P.	
XX	13-OCT-1999; 99US-0159122P.	
XX	(GORI/) GORING D.	
XX	(SILV/) SILVA N.	
XX	Goring D, Silva N;	
XX	WPI; 2001-244305/25.	
XX	New proline-rich, extensin-like receptor kinase nucleic acids and	
XX	polypeptides useful for increasing plant wounding or pathogen resistance,	
XX	or for producing transgenic plants with increased wounding or pathogen	
XX	resistance.	
XX	Claim 6; Fig 1; 91pp; English.	
XX	The present invention relates to proline-rich extensin-like receptor	
XX	kinase (PERK). The PERK nucleic acids and polypeptides are useful for	
XX	increasing the resistance of plants to wounding and pathogens. These are	
XX	also useful for producing transgenic plants with increased wounding and	
XX	pathogen resistance compared with a wild type plant, as well as in assays	
XX	for identifying and developing compounds to inhibit and/or enhance	
XX	polypeptide function directly	

XX Sequence 1944 BP, 464 A, 550 C, 459 G, 471 T, 0 U; 0 Other;
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 Best Local Similarity 100.0%; Pred. No. 0;
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 DB 1441 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1501 GGAAGCTTTGAGAGGTTTATGCTGATGATGATGATGATGATGATGATGATGATG 1560
 DB 1501 GGAAGCTTTGAGAGGTTTATGCTGATGATGATGATGATGATGATGATGATGATG 1560
 QY 1561 GCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 DB 1561 GCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 QY 1621 ATGAGCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 DB 1621 ATGAGCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 QY 1681 ATGAGCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 DB 1681 ATGAGCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 QY 1741 AGCCAGTACATGAG 1800
 DB 1741 AGCCAGTACATGAG 1800
 QY 1801 AAGCCAGAGGAGTATGATATGATATGATATGATATGATATGATATGATATGATATG 1860
 DB 1801 AAGCCAGAGGAGTATGATATGATATGATATGATATGATATGATATGATATGATATG 1860
 QY 1861 AAGCCAGAGGAGTATGATATGATATGATATGATATGATATGATATGATATGATATG 1920
 DB 1861 AAGCCAGAGGAGTATGATATGATATGATATGATATGATATGATATGATATGATATG 1920
 QY 1921 GGTATATGATGAG 1980
 DB 1921 GGTATATGATGAG 1980

RESULT 2
 ACF36548
 ID ACF36548 standard; cDNA; 1944 BP.
 XX ACF36548;
 AC ACF36548;
 XX


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Db      1261 GCTAAATTCCTTCTATACAAACGCGATGATCAACGCTGATGGGAACCTTTGGG 1320
QY      1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAGCTCAACGGAAGTCTGACGTTTCTCA 1380
Db      1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAGCTCAACGGAAGTCTGACGTTTCTCA 1380
QY      1381 TTTGGCGTGTGCTTTTGGAGCTCATTAATGAGCGTGCAGCCGCTGATGCGCAACATGTC 1440
Db      1381 TTTGGCGTGTGCTTTTGGAGCTCATTAATGAGCGTGCAGCCGCTGATGCGCAACATGTC 1440
QY      1441 TATGTAGATGACAGCTTAGTGAAGTGGGACGACCATTTGCTTAAACGAGCATCTGACAA 1500
Db      1441 TATGTAGATGACAGCTTAGTGAAGTGGGACGACCATTTGCTTAAACGAGCATCTGACAA 1500
QY      1501 GGAAGACTTTGAGGGTTTAACTGATGCAAGATGATATATGGGTATGACAGAGAGAGATG 1560
Db      1501 GGAAGACTTTGAGGGTTTAACTGATGCAAGATGATATATGGGTATGACAGAGAGAGATG 1560
QY      1561 GCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db      1561 GCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY      1621 ATGAGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db      1621 ATGAGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY      1681 ATGAGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db      1681 ATGAGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY      1741 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db      1741 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
QY      1801 AACCCCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
Db      1801 AACCCCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
QY      1861 AGCAGCGAGGCGCCAAACCAACGCGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 1920
Db      1861 AGCAGCGAGGCGCCAAACCAACGCGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 1920
QY      1921 GGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1944
Db      1921 GGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1944

RESULT 3
ACF36549
ID      ACF36549 standard; cDNA; 2189 BP.
XX      ACF36549;
AC      18-DEC-2003 (first entry)
DT      18-DEC-2003 (first entry)
XX      B. napus PERK1 receptor kinase encoding cDNA.
DE      PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
XX      wound; pathogen resistance; plant growth; seed production; gene; ss.
XX      Brassica napus.
XX      Key Location/Qualifiers
FH      1.2189
FT      C
FT      /note="ABR82938; this protein contains the amino acids
FT      corresponding to 5' and 3' UTR regions, though only the
FT      relevant aa residues (ABR82937) is used in the invention"
FT      5'UTR 1..96
FT      /tag= a
FT      CDS 97..2040
FT      /tag= b
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FT      /transl_except= {pos: 1332, .1334, aa: Phe}
FT      /product= "PERK1"
FT      /note= "ABR82937; proline-rich Extensin-like Receptor
FT      Kinase"
FT      3'UTR 2041..2189
FT      /tag= a
XX      WO2003072763-A1.
XX      04-SEP-2003.
XX      28-FEB-2003; 2003WO-CA000274.
XX      28-FEB-2002; 2002CA-02373903.
XX      28-FEB-2002; 2002US-00086464.
XX      (GORI/) GORING D.
XX      PA (SILV/) SILVA N. Z.
XX      PA (HAFF/) HAFFANI Y. Z.
XX      Goring D, Silva N, Haffani YZ;
XX      WPI: 2003-712727/67.
XX      P-PSDB; ABR82937, ABR82938.
XX      Producing a transgenic plant having an increased plant resistance, plant
XX      growth or seed production comprises transforming a plant with a nucleic
XX      acid molecule having a Proline-rich Extensin-like Receptor Kinase
XX      activity.
XX      Disclosure; Fig 1D; 123pp; English.
XX      The invention relates to producing a transgenic plant having increased
XX      plant height, number of branches, number of seed pods and/or seed
XX      production compared to a non-transgenic plant, and/or quicker flowering
XX      or later senescence compared to a non-transgenic plant. The method
XX      involves transforming a plant with a vector including a Proline-rich
XX      Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
XX      acid molecule having PERK activity. The method, as well as the PERK
XX      nucleic acid molecule and polypeptide, are useful in increasing plant
XX      resistance to wounding and pathogens and in increasing plant growth and
XX      seed production. The nucleic acid molecule and polypeptide may also be
XX      used in producing transgenic plants or transgenic host cells. The present
XX      sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
XX      polypeptide
XX      Sequence 2189 BP; 544 A; 592 C; 494 G; 559 T; 0 U; 0 Other;
XX      Query Match 100.0%; Score 1944; DB 10; Length 2189;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ATGTCTCGGCGCGCTCTCCG3GAGTGGTTGCGCTTCATCTCCACATCAAACTCCACA 60
Db      97 ATGTCTCGGCGCGCTCTCCG3GAGTGGTTGCGCTTCATCTCCACATCAAACTCCACA 156
QY      61 ACCACCACTCTCTCTCAAGCTTCTGCTCTCTCTCCACACACCTTTCTCTCCGCGG 120
Db      157 ACCACCACTCTCTCTCAAGCTTCTGCTCTCTCTCCACACACCTTTCTCTCCGCGG 216
QY      121 CCATCCATATTTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db      121 CCATCCATATTTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276
QY      217 CCATCCATATTTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db      181 CCATCCATCAACCACTTCATAGCGCGGATCTCCACCTCTCTCTCTCTCTCTCTCTCTCA 240
QY      277 CCATCTCCACCAAGCTTCATAGCGCGGATCTCCACCTCTCTCTCTCTCTCTCTCTCTCA 336
Db      241 CCGGCTCCAACTAGCGCGGATCTCCACCGGACCTGTTACTCTCTCTCTCTCTCTCTCTCTCT 300
QY      337 CCGGCTCCAACTAGCGCGGATCTCCACCGGACCTGTTACTCTCTCTCTCTCTCTCTCTCTCT 396
Db      301 CCACTTCAAGTCCCGAGGACCAACCGCTCAATCTCTTCAAGGAGAGATCTCTCTGACCT 360
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Db      397  CCACCTTCAGTCCACAGGACCAACGTCCTCAATCTTCAAGCAGAGAGATTTCTCCAGACT 456
Qy      361  CCATCTTCTCCCTCGCCGCGTCTCTCTTCTTCCAGCGTTTAAACAGAGATGTGTG 420
Db      457  CCATCTTCTCCCTCGCCGCGTCTCTCTTCTTCCAGCGTTTAAACAGAGATGTGTG 516
Qy      421  GGAATGCCCATCGGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db      517  GGATGCGCATCGGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576
Qy      481  AAGAGAAAACGACGAGAGACGAAGAAGATCTTACATGTCTCTCGACCTCTCTCT 540
Db      577  AAAAAAAGAGAGAGAGAGAGAGAGAGATCTTACATGTCTCTCGACCTCTCTCT 636
Qy      541  GGTCCAAAAGCCGAGAGACCTTAACGTTGACACAGACCAACATGCGGCAACAAA 600
Db      637  GGTCCAAAAGCCGAGAGACCTTAACGTTGACACAGACCAACATGCGGCAACAAA 696
Qy      601  AACACCCGCTCAGATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db      697  AACACCCGCTCAGATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 756
Qy      661  CCACGGCAACCTCTCCACCTCCACACCGCTTTGATGAGAGAGAGAGAGAGAG 720
Db      757  CCACGGCAACCTCTCCACCTCCACACCGCTTTGATGAGAGAGAGAGAGAGAG 816
Qy      721  TACTGGAACCGTCCAGTTCTTCTCCACCGTCTCCAGGCTTGTGTGTGTGTGT 780
Db      817  TACTGGAACCGTCCAGTTCTTCTCCACCGTCTCCAGGCTTGTGTGTGTGTGT 876
Qy      781  AACACCTTTCACATACAGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db      877  AACACCTTTCACATACAGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 936
Qy      841  TTAGGACAAAGCGGAGTTACGTTACGTTACGTTACGTTACGTTACGTTACGTT 900
Db      937  TTAGGACAAAGCGGAGTTACGTTACGTTACGTTACGTTACGTTACGTTACGTT 996
Qy      901  GGTGTGAACAGTTGAAAGTTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
Db      997  GGTGTGAACAGTTGAAAGTTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1056
Qy      961  GAGATATATAGACAGATGTACCAACAGGATGTGTGTGTGTGTGTGTGTGTGT 1020
Db      1057  GAGATATATAGACAGATGTACCAACAGGATGTGTGTGTGTGTGTGTGTGTGT 1116
Qy      1021  GGTGCCAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
Db      1117  GGTGCCAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1176
Qy      1081  CATGCGAGAGAGCGGCTTAAATGAGATGAGACACCAAGATGAGATGAGATG 1140
Db      1177  CATGCGAGAGAGCGGCTTAAATGAGATGAGACACCAAGATGAGATGAGATG 1236
Qy      1141  GGTAAAGAGCTTTTATATCTTATGAAAGTTGCAATCTTAAATCACTTACGTA 1200
Db      1237  GGTAAAGAGCTTTTATATCTTATGAAAGTTGCAATCTTAAATCACTTACGTA 1296
Qy      1201  AAGGCTTCAACATATGATGATTTCAAGTTGAAAGTGAAGTGTGTGTGTGTGT 1260
Db      1297  AAGGCTTCAACATATGATGATTTCAAGTTGAAAGTGAAGTGTGTGTGTGTGT 1356
Qy      1261  GCTAAGATTTGCTTGTATCAAAACAGATGTATCAACAGTGTGTGTGTGTGT 1320
Db      1357  GCTAAGATTTGCTTGTATCAAAACAGATGTATCAACAGTGTGTGTGTGTGT 1416
Qy      1321  TACTGGCTCCGGAATAGCTGTGAAGCGAAGATGTGAAGATGTGTGTGTGTGT 1380
Db      1417  TACTGGCTCCGGAATAGCTGTGAAGCGAAGATGTGAAGATGTGTGTGTGTGT 1476
Qy      1381  TTTGGGTTGTGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440

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Db      1477  TTTGGGTTGTGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1536
Qy      1441  TATGTAGATGACAGCTTATGTGACGTGGGACGACCAATGCTTAACGAGCATGT 1500
Db      1537  TATGTAGATGACAGCTTATGTGACGTGGGACGACCAATGCTTAACGAGCATGT 1596
Qy      1501  GAGACTTTGAGGGTTTACCTGATGCAAAAGATGAAATGATGATGATGATGATG 1560
Db      1597  GAGACTTTGAGGGTTTACCTGATGCAAAAGATGAAATGATGATGATGATGATG 1656
Qy      1561  GCTCGATGTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Db      1657  GCTCGATGTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1716
Qy      1621  ATGAGCAGATTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Db      1717  ATGAGCAGATTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1776
Qy      1681  ATGAGCAGATTTCAAAAGATGATACAGCTCATACGAGAGAGACCGATTAATGA 1740
Db      1777  ATGAGCAGATTTCAAAAGATGATACAGCTCATACGAGAGAGACCGATTAATGA 1836
Qy      1741  AGCGAGTAAATGAAAGACATGAAAGATTTAGAAATGACCTTGAATCAAGTAC 1800
Db      1837  AGCGAGTAAATGAAAGACATGAAAGATTTAGAAATGACCTTGAATCAAGTAC 1896
Qy      1801  AAGCGACGGGTGAGTACAGTATCCGACAGTATGATGAGTGTGTGTGTGTGTGT 1860
Db      1897  AAGCGACGGGTGAGTACAGTATCCGACAGTATGATGAGTGTGTGTGTGTGTGT 1956
Qy      1861  AGCAGGAGGGCCAAACCAACAGCGAAATGAGATGAGAGATTTAAGAAACCGGT 1920
Db      1957  AGCAGGAGGGCCAAACCAACAGCGAAATGAGATGAGAGATTTAAGAAACCGGT 2016
Qy      1921  GGTATATGAGACCTTCTCTTAA 1944
Db      2017  GGTATATGAGACCTTCTCTTAA 2040

RESULT 4
ACF36557
ID   ACF36557 standard, DNA; 1959 BP.
XX
AC   ACF36557;
XX
DT   18-DEC-2003 (first entry)
XX
DE   A. thaliana PERK1 protein encoding genomic DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
XX   wound; pathogen resistance; plant growth; seed production; gene; ds.
XX   Arabidopsis thaliana.
OS   Arabidopsis thaliana.
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003MO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
XX
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
XX   (SILV/) SILVA N.
XX   (HAFF/) HAFANI Y Z.
XX
PI   Goring D, Silva N, Hafani YZ;
XX
DR   MPI; 2003-712727/67.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
XX   growth or seed production comprises transforming a plant with a nucleic

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PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.

PS Disclosure; Fig 21d; 123pp; English.

XX The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC and resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents an A. thaliana PERK1 DNA (At3g24550)

SQ Sequence 1959 BP; 496 A; 514 C; 425 G; 524 T; 0 U; 0 Other;

Query Match 70 4%; Score 1369.4; DB 10; Length 1959;

Best Local Similarity 83.4%; Pred. No. 0; Mismatches 291; Indels 30; Gaps 4;

Matches 1611; Conservative 0; Mismatches 291; Indels 30; Gaps 4;

QY 31 TCGCTCCATCTCCACATCAAACTCCAAACACACACTCTCTCCACAGCTTCCGCTCT 90
DB 40 TCTCCACGCTCTCCCTCCCAAACTCGAACACACACTCTCTCCACAGCTCTTCT 99
QY 91 CTTCCACCAAC-----CTTCTCTCTCTCGCGCGCATTCAGTATTCGACATCT 141
DB 100 CTTCTCCACCAACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 159
QY 142 CTTCT 201
DB 160 CTTCT 219
QY 202 ACGCGGAGATCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261
DB 220 A-----CT 267
QY 262 TCTCCACCGCAGCT 321
DB 268 CCACGCTCTCCACCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 327
QY 322 CCGTCCATCT 381
DB 328 CCAACACT 387
QY 382 TCT 441
DB 388 TCTGATCT 447
QY 442 GCT 498
DB 448 GCTATCT 507
QY 499 ---GAAG 555
DB 508 CAGGAG 567
QY 556 GAGCTTACGATGAG 615
DB 568 GAGCTTACGATGAG 627
QY 616 CATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 675
DB 628 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687
QY 676 ---CCAGCTTACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
DB 688 CCGGCTTACGATGAG 747
QY 733 CCAATTTCT 792

DB 748 CCGGCTTCT 807
QY 793 TAG 852
DB 808 TATAG 867
QY 853 GGGTTCCGTTACGTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 912
DB 868 GGGTTCCGTTACGTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 927
QY 913 TTGAAG 972
DB 928 TTGAAG 987
QY 973 AGAGTTACCAAG 1032
DB 988 AGAGTTACCAAG 1047
QY 1033 TTGCTTGTCTATGAG 1092
DB 1048 TTACTTGTCTATGAG 1107
QY 1093 CCGCTTACATGAG 1152
DB 1108 CCGCTTACATGAG 1167
QY 1153 TCTTATCTTCTATGAG 1212
DB 1168 TCTTATCTTCTATGAG 1227
QY 1213 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1272
DB 1228 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1287
QY 1273 TCTGATTAACACGAG 1332
DB 1288 TCTGATTAACACGAG 1347
QY 1333 GAATAGCTGCAAG 1392
DB 1348 GAATAGCTGCAAG 1407
QY 1393 CTTTGAAGCTTATCTGAG 1452
DB 1408 CTTTGAAGCTTATCTGAG 1467
QY 1453 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1512
DB 1468 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1527
QY 1513 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1572
DB 1528 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1587
QY 1573 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1632
DB 1588 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1647
QY 1633 GTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1692
DB 1648 GTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1707
QY 1693 CAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1752
DB 1708 CAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1767
QY 1753 GAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1812
DB 1768 GAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1827
QY 1813 GAGTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1872

Db 1828 GAGTACAGTAAATCCACGACGTGACTACCGCTGCTGCTTCAAGCAGTGAAGT 1887
QY 1873 CAACACACGCGCAATGAGATGGGGAAGATTAGAGAACCGGCTCAGGTTATAGTGA 1932
Db 1888 CAAAGCCACGAGAAATGAGATGGGAAAGATTAAAGAAACCGGTCAAGGTTATAGTGA 1947
QY 1933 CCTTCTCTTTAA 1944
Db 1948 CCTCTCTTTAA 1959
RESULT 5
AAC6968
ID AAC6968 strand; DNA; 2324 BP.
AC AAC6968;
XX 17-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 15710.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-00301439.
PF
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
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PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 10-JUN-1999; 99US-0138540P.
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PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
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PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
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PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 22-JUL-1999; 99US-0145192P.
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PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
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PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
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PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.

PR 09-AUG-1999; 99US-0147935P
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PR 13-AUG-1999; 99US-0148684P
PR 16-AUG-1999; 99US-0149368P
PR 17-AUG-1999; 99US-0149375P
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PR 25-AUG-1999; 99US-0150566P
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PR 15-SEP-1999; 99US-0154018P
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PR 28-OCT-1999; 99US-0161920P
PR 28-OCT-1999; 99US-0161922P
PR 28-OCT-1999; 99US-0161933P
PR 29-OCT-1999; 99US-0162142P

Query Match 69.0%; Score 1341.2; DB 3; Length 2324;
Best Local Similarity 82.8%; Pred. No. 8.9e-309;
Matches 1598; Conservative 0; Mismatches 303; Indels 28; Gaps 5;

31 TCGCTCATCTCCACCATCAAACTCCACACCACTCTCTCTCCAGCTTCGCTCTCT

Db 144 TCTCCACCGCTCTCTCCACAACTCGACACACCACTCTCTCTCAGAGCTCTCT 203
Qy 91 CCTCCACCAAC-----CTTCTCTCTCCGCGCGCATCTCACTATTCGACATCT 141
Db 204 CTTCTCTCCACCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 263
Qy 142 CTTCT 201
Db 264 CTTCT 323
Qy 202 AGCGCGGATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261
Db 324 A-----CT 371
Qy 262 TCTCCACCGCGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321
Db 372 CCGCGCTCTCTCCACACACCTCTCAACCTCTGAAAGCTCTCTCTCTCTCTCT 431
Qy 322 CCGTCCATCTCTCTCAGCAGAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCT 381
Db 432 CCAAGACTCTCTCAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491
Qy 382 TCT 441
Db 492 TCTGATCT 551
Qy 442 GCT 498
Db 552 GCTATCT 611
Qy 499 GACGAGAGATCT 558
Db 612 CAGACGATGAGCT 671
Qy 559 CTTTACGCTGAGCAGCAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
Db 672 CTTTACGCTGATCAACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 731
Qy 619 GTCTGAGCT 675
Db 732 CATGATGAGCT 791
Qy 676 CCACCTCCACACCGCT 735
Db 792 CCACCTCCACACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 851
Qy 736 GTTCT 795
Db 852 GTTCT 911
Qy 796 GAGAGCTAGCTAGACCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
Db 912 GAGAGCTGTGAGAGCTACTATAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 971
Qy 856 TTCTGTTACGTGACAAAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 915
Db 972 TTCTGTTATGTCATAAAGTATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1031
Qy 916 AAAGTTGGAGATGTCAGAGAGAGAGAGTTCTCTCTCTCTCTCTCTCTCTCTCT 975
Db 1032 AAAGCTGAGAGGTCAGAGAGAGAGAGTTCTCTCTCTCTCTCTCTCTCTCTCT 1091
Qy 976 GTTTCACACAGGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1035
Db 1092 GTTTCATCAGGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1151
Qy 1036 CTTGCTATGAGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1095
Db 1152 CTTGCTATGAGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1211
Qy 1096 CTTACATGAGATGAGACCAAGATTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1155

QY	1095	CGGCCCTAAATGGAAATGAGACACCAAGTTGATCTCTTGAGATCGCTAAAGAGCTT	1152
Db	463	CGACCAACAATGGAGTGCCCTGCTAGTTAAAGTCAAGTTGGGTGTCGCAAGGGTTTA	522
QY	1153	TCTTAATCTTANTGAGAAGTTGCATCTCTAAATCAATTCACCGGTATATCAAAGCTTCAAC	1212
Db	523	GCATTATCTTCATGAAAGCTGCATCCAAAGATCATTCATCGTGCATAAAGGCATCTAAC	582
QY	1213	ATATGTATAGATTTCAAGTTTGAAGCTTAAGTGTCTGATTTTGGTCTTGGTAGATTGCT	1272
Db	583	ATTCTCTTTTACCTTCCAAATTTGAAAGCTTAAGGTGTCTAATTTTGGACTCGAAGATTACT	642
QY	1273	TCTGATCAAAACACGCAATGTATCAACACGTTGTGATGGAAACCTTTGGGTACTTGGCTCCG	1332
Db	643	ACTGATATAACAACACCCCATGTTATCGACAAGATATGGGACCTTTGGGTATTTTGGACCT	702
QY	1333	GAATAGCCTGCAAGCGGAAAGCTCAACGAGAGATCTGAAGTCTGACTTTTCTATTTTGGCGTTGTG	1392
Db	703	GAGATGCATCTTCTGCGCAAGCTTAACGAAAAATCCCATGTATTTCTCTTCGAGGTATG	762
QY	1393	CTTTTGAAGCTCAATTAATCGACGTCGACCGCTGTATGCGAACATATGCTATGTAGATGAC	1452
Db	763	CTTCTTGAGCTTATTAATCTGGCGCGACGACATATACACACCCAAACATATATGATGAC	822
QY	1453	AGCTTAGTGTACTGGGACACGACCAATGCTTAACCGAGATCTGACAAAGAGACTTTGAG	1512
Db	823	AGCTTGTGTACTGGGCAAGGCCATTTACTGATGGAGACCTTGAAGATGGTAATATGAT	882
QY	1513	GGTTTAGCTGACAAAGATGATATATATGGTATGACAGAGAGAGATGGCTCGATGGTT	1572
Db	883	GCTTTAGTGAATCTCGGCTGGGAAAGACTTCAATCTTATGAGATGGCAAGATGATA	942
QY	1573	GCTTGTGTGCGGGCTGTGTGCGCATTCAGCTCGCCGACACTCGCATGAGCCAGATT	1632
Db	943	GCGTGTGAGCTGCATGTATGCGCATTTCTGCACTGTGTGCGCACGTTATGATGACAGTTC	1002
QY	1633	GTGCGTGCCTTAGAAGAGAAATGATCACTGTCAAGTCTTAAAGAAAGGATGAGACAGGT	1692
Db	1003	GTTGGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAAATGAAGTGTTCGGCTGTGC	1062
QY	1693	CAAGCAATGTATACAGCTCATACGAGAGAAAGACCCGATTTAGTCTGAGCGCATGATCAT	1752
Db	1063	CATAGCCGCTTCTTTGGGTCAATAC---AGCAGCTTCGATTCAGATTCGGCCAGTACAC	1115
QY	1753	GAAAGCATGAAGAAGTTTAGGAAATGGCACTTGGAATCAAGAGTACACGCCACGGGT	1812
Db	1120	GAGGACATGAAGAAGTTCAAGAGATGGCAATTTGCAAGAGTACACGCCACGGGT	1172
QY	1813	GAGTACAGTAATCCGACCAAGTACTATGAGACTGTACCCGCTGTGTTCAAGCAGCAGGGC	1872
Db	1174	CAATACAGGCGCCCAACCAAGTAAATATGACAGATACCGTCTGCAATCAAGCGCAGGGC	1232
QY	1873	CAAAACCAACGCGAATATGAGATGGGGAAAGATTATAGAGAACCGGTCAAGGTATATAG	1928
Db	1234	CACCAAGCGCAAGAGATGAGTCGGGTGCATGAAGAAAGGTGGCTACAGTGTGG	1289
RESULT 7			
ACF36556			
ID ACF36556 standard, DNA; 1488 BP.			
AC ACF36556;			
XX 18-DEC-2003 (first entry)			
XX G. max PERK partial EST sequence.			
XX PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;			
XX wound; pathogen resistance; plant growth; seed production; soybean; gene;			
XX ds.			
XX Glycine max.			
OS			

[illegible]

Db 847 GTTGTTATGATGATTTCTGGAGGGAAGAGTGTGTTGTCTATGATGATGTTGCCAAACAC 906
 Qy 1063 AATCTCGAGCTTCACTCCATGCGAGGAGCGGCTTACATGAAATGAGACACAGATTTG 1122
 Db 907 ACATTGGAGCTCCACTTGATGGAGAGGCGACCAACATGAGATGAGCTTACAGATTA 966
 Qy 1123 AAGATTGCTTGGATCTGCTAAAGACTTCTTATCTTCATGAAAGATTTGCAATCTTAAA 1182
 Db 967 CGCATTTGCTTTGGGCTGCGAAGGAGTTGGCATATCTTCTTGAAGATTTGCCATCTTAA 1026
 Qy 1183 ATCATTCACCGTATATCAAGGCTTCAAAACATTTGATGATTTCAAGTTGAAGCTTAA 1242
 Db 1027 ATCATTCACCGTATATCAAGGCTTCAAAACATTTGATGATTTCAAGTTGAAGCTTAA 1086
 Qy 1243 GTTGCTGATTTTGGCTTCTGCTAAAGTCTTCTGATACAAACAGGCACTGATCAACAGT 1302
 Db 1087 GTGCGAGATTTGCGACTTGAATAATGACTTCTGTATTAACACTCATGTTTCAACAG 1146
 Qy 1303 GTGATGGGACCTTTGGTACTTGGCTCGGAAATACGCTGCAAGCGGAAAGCTCAAGAG 1362
 Db 1147 GTATGGACATTTGGTACTTGGCTCGGAAATACGCTGCAAGCGGAAAGCTCAAGAG 1206
 Qy 1363 AAGTCTGACGTTTCTCATTTGGCGCTTGTGCTTTGAGCTCATTAAGCTGACGCTCC 1422
 Db 1207 AATCATGATGCTTTCTTTTGGAGTAAATGCTTTGAGCTAAATACGCTGCGCGCTCT 1266
 Qy 1423 GTTGATGCGAACATGCTATGATGATGACAGCTTATGATGAGCTGCGACACACATTTGCT 1482
 Db 1267 GTGAGATGAAACCAATCAACATGATGACAGCTTGTGATGAGGCAAGGCTTTTAAATG 1326
 Qy 1483 AACGAGCATCTGAGCAAGAGACTTTGAGGCTTATGAGCTGATGCAAAATGAAATATGAG 1542
 Db 1327 ATGCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1386
 Qy 1543 TATGACAGAGAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1602
 Db 1387 TACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1446
 Qy 1603 GCTGCGCCGACACTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1662
 Db 1447 GACGCTCGACCGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1506
 Qy 1663 TCAGATCTTAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1722
 Db 1507 GATGATCTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1563
 Qy 1723 AGCAGCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1782
 Db 1564 AGCAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1623
 Qy 1783 CTGGAAGCT 1791
 Db 1624 TTGAGCAAGT 1632

RESULT 9

ADK53814 standard; DNA; 685 BP.

ADK53814;

06-MAY-2004 (first entry)

Plant DNA sequence which confers altered metabolic characteristic #1197.

DE altered metabolic characteristic; plant; acid metabolism;
 KW alcohol metabolism; fatty acid metabolism;
 KW branched fatty acid metabolism; alkaloid metabolism;
 KW amino acid metabolism; ester metabolism; glyceride metabolism;
 KW phenolic metabolism; carbohydrate metabolism; steroid metabolism;
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

KW quinine metabolism; disease resistance; gene shuffling; sexual PCR; ds.
 OS unidentified.
 XX WO2003020936-A1.
 XX 13-MAR-2003.
 XX 30-AUG-2002; 2002WO-US027884.
 XX 31-AUG-2001; 2001US-0316471P.
 XX (DOMC) DOM CHEM CO.
 XX (DOMC) DOM AGROSCIENCES LLC.
 XX Weglarz T, Gachotte P, Blakeslee B, McCreary DA, Pell RJ,
 XX Orredo JVB, Croxley R, Reddy AS, Shukla V, Lattinua I, Miller BA;
 XX WPI; 2003-313091/30.
 DR Novel genes that confer altered metabolic characteristics in Nicotiana
 XX benthiana plants, useful for altering the levels of metabolites e-9.
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
 PS Claim 1; SEQ ID NO 1197; 2576bp; English.
 CC The invention comprises DNA sequences which confer an altered metabolic
 CC characteristic when they are expressed in a plant. The DNA sequences of
 CC the invention are useful for producing plants with an altered metabolic
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,
 CC altered glyceride metabolism, altered phenolic metabolism, altered
 CC carbohydrate metabolism, altered steroid, oxygenated terpene, or
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
 CC metabolism, ketone or quinine metabolism. The DNA sequences of the
 CC invention may be used to provide disease resistance in a plant and gene
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a
 CC DNA sequence of the invention.
 SQ Sequence 685 BP; 181 A; 130 C; 176 G; 197 T; 0 U; 1 Other;

Query Match 16.9%; Score 329.2; DB 10; Length 685;
 Best Local Similarity 68.8%; Pred. No. 4.1e-68;
 Matches 467; Conservative 0; Mismatches 209; Indels 3; Gaps 1;

Qy 923 GAGTGTCTCAGGAG 982
 Db 10 GAGAGCGGAAAGGAG 69
 Qy 983 ACAGGATCTGGTGTCTCTTGTGATTTATGATGATGATGATGATGATGATGATGATGATG 1042
 Db 70 ATGCGATTTGTTTCACTCGTGTGATTTATGATGATGATGATGATGATGATGATGATGAT 129
 Qy 1043 ATGAGTTTGTCTTAAACAATCTCGAGCTTACCTTCATGCGAGAGAGAGAGAGAGAG 1102
 Db 130 ATGACTATGATGCGAGACACACATCTGATCATCTTCACTGATGAGAGAGAGAGAGAG 186
 Qy 1103 TGGATGAG 1162
 Db 187 TGGATGAG 246
 Qy 1163 ATGAGATTTGCAATCTTAAATCATCTTCACTGATGATGATGATGATGATGATGATGAT 1222
 Db 247 ATGAGATTTGCAATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 306
 Qy 1223 ATTTCAAGTTGAG 1282
 Db 307 ATATCAACTTTGAG 366
 Qy 1283 ACAGGATGATCAACAG 1342
 Db 367 ATACACATGTGTCACTGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426

PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155466P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158028P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
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PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.

PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 11.1%; Score 215.8; DB 3; Length 1703;
Best Local Similarity 59.0%; Pred. No. 5.6e-41;
Matches 430; Conservative 0; Mismatches 287; Indels 12; Gaps 3;

QY 769 GGCTTCACAAAACACTTTCACATAGAGAGTACTAGAGCCACCAATGGTTCTCC 828
DB 209 GCATCTCAGCGCAAACTTTCACCTTCGAGGCTTCCTACCGCACAGAACTTACG 268
QY 829 GAGCGCAACTTGTAGACAAAGCGGCTTGTACCTGCACAAAGTG--TGTTCCT 885
DB 269 CCCAGTCTTCCTCGSAGAGGAGGTTTGGAGTGTATTAAGAGGCGGCTTGAAGC 328
QY 886 AGTGGAAAGAGTGTCTGAGACACTTGAAGTTGAGAGTGTGAGAGAGAGG 945
DB 329 ACAAGCAGGTTGTCTATTAAGCAGCTTAAAGGATGGGCTTCAAGAAAGAGAA 388
QY 946 TTTCAGCAGAGTTGAGATCATCAGACAGTTACACAGGCATCTGTCTTGT 1005
DB 389 TTCTGTAGAGAGTTCTCATGCTCAGCTTACTACATCATCAAACTGTATTTGAT 448
QY 1006 GGTATTGCAATCGCGGTGCGCAAAAGATTGCTCTATGAGTTTGTCTTACACAA 1065
DB 449 GGTATTGTGTGTATGAGACAGACAGACTTCTTTATGAAATATAGCTTGTGATCA 508
QY 1066 CTCGAGCTTCACTCCATGCGGAGGAGCGGCTT-----CAATGATGAGACCA 1119
DB 509 CTTGAAATCATTTTGACGATCTACCTTGTATTAAGAGGCTTGTGAGACCAAG 568
QY 1120 TTGAAGATGCTCTTGATCTGTAAGAACTTCTTATCTTCAATGAAATTCATCT 1179
DB 569 ATGAAATTTGACAGAGTGTCTGCCAAGAGCTGAGTACTTCAATGAAAGCTTATCA 628
QY 1180 AAATTCATTCACCGTATATCAAGGCTTCAAAATATGATGATTTCAAGTTGAAG 1239
DB 629 CCACTTATTTATAGGATTTCAAGTCAATGCAAACTTGTGATGAAATTTCCACCG 688
QY 1240 AAGTTGCTGATTTTGTCTTGTCTGTAAGATTCCTTCTATCAAA--CGCATGTATCA 1296
DB 689 AAGCTGTCTGATTTTGGACTGCTAAGTGTGTCAGAGTGCACAAATCACATGTCTCA 748
QY 1297 ACAGGTGATGGGACCTTTGGTACTGTGCTCGGAATACGCTGCAGAGGAAAGCTC 1356
DB 749 ACACGTATATGGTATCATATGTTATTTGTACACAGAAATATGCTATACAGGGACGTG 808
QY 1357 ACAGGAAGTCTGACGTTTCTCATTTTGGCGTGTGCTTTTGAAGCTTACTGAGCGT 1416
DB 809 ACAGTGAAGTCTGACGTTATATGTTTGGGTTGTCTTGTAGAGTTACTGAGCGGT 868
QY 1417 CGACCCGTTGATGCAACAATGTCTATGATGATGACGCTTATGTTGATGGGACGACCA 1476
DB 869 AGGCTATTTGACACACACAGACCAATGAGAAACAAATCTTGTCTCAATGGGACGTTCT 928
QY 1477 TTGCTTAAAC 1485
DB 929 CTGTTTAAAC 937

RESULT 11
AAC43029 ID AAC43029 standard; DNA; 1419 BP.
XX AAC43029;
AC 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 37767.
DE
XX

KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS EPI033405-A2.
XX
XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-012180P.
PR 09-MAR-1999; 99US-0123546P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
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PR 18-MAY-1999; 99US-0134768P.
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Query Match 10.5%; Score 204.6; DB 3; Length 1419;
 Best Local Similarity 57.2%; Pred. No. 2,4e-38;
 Matches 394; Conservative 0; Mismatches 289; Indels 6; Gaps 1;

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DB 436 GAGGTTAAGCGCGCAAGATGGGCTTTGTAAGAGATGTAATCGAGAGAGGTGTTAC 495
QY 859 GGTACGTGCAAAAGGTGTGTTGCTAGTGGAAAGTGTGTGAAGCAAGTTGAA 918
DB 496 GGGATTGTGATCGTGCATTTTAACTGATGGAACAAAGTCGCGTCAGAACTTCTT 555
QY 919 GTTGGAGGTGTGTCAGGAGAGAGGAGTTTCAGCAAGGTTGATCATCAGAGGCTT 978
DB 556 AACAAATAGGGGTCAAGAGAGAGAAATTCAAATGAGAGTCAATTCATTGGCGAGTA 615
QY 979 CACACAGGATCTGGGTCTCTTGTGTTATGATCGCGGTGCAAAAGTTGCTT 1038
DB 616 CGAACACAGATCTTTAGGCTTTTAGGGATTGCGTGAAGTGATTCAGAGATGCTC 675
QY 1039 GTCTATAGTTGTTCTTAACACAAATCTCGAGC-----TTCACTTCATGGCGAGGGA 1092
DB 676 GTGATACCTTTTGCGAACAAATGTAATTTGAGCAATGATTCACGGTGAATGTTGGGAT 735
QY 1093 CGGCTTAACAAATGAGAGAGACCAAGATGGAAGTTGCTTGGATCTGCTAAAGACTT 1152

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DB 736 GTCACCCGCTAACTTGGGATATAGTATGATATTAATTAAGGAGATGCCAAGATTG 795
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DB 796 GCGTATCTACAGAGGCTTTAGCGCAAAAGTTGCTTACGGGATATTAATCAAGCAAT 855
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QY 1273 TCTGATACAAACAGATATATCAACAGTGTGATGGAAGCTTTGGGACTTGCTCG 1332
DB 916 GGGTCGAGAGAGATTATGTACTCTGATGATGGAACCTTCGTTATGAGACCA 975
QY 1333 GATAAGCTGCAAGCGGAAAGCTCAAGAGTCAAGTCAAGTTTTCATTTGGCGTTGTG 1392
DB 976 GAAATAGCTTGACCGGATATGTTAAACGAAAGATGATATATAGTTCGGAATAGTA 1035
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QY 1453 AGCTTAGTGAAGTGGGACAGACCATTCCT 1481
DB 1096 ATCTAGTGAATGGCTTAATCATGCT 1124

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RESULT 12
 ABZ13121
 ID ABZ13121 standard; DNA; 1419 BP.
 XX ABZ13121;
 AC 21-JAN-2003 (first entry)
 XX
 DT Arabidopsis thaliana stress regulated gene SEQ ID NO 926.
 XX
 DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 EN W0200216655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001MO-US026685.
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 PR 24-AUG-2000; 2000US-0227666P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 PA (SCRI) SCRIpps RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PT Harper JF, Kreps J, Wang X, Zhu T;
 FI WPI; 2002-304127/34.
 XX
 DR Identifying a stress condition to which a plant cell has been exposed and
 XX producing plants with increased tolerance to these abiotic stresses.
 PT
 PT Claim 144; SEQ ID NO 926; 577BP + Sequence Listing; English.
 PS
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 1419 BP; 387 A; 272 C; 401 G; 359 T; 0 U; 0 Other;

Query Match 10.5%; Score 204.6; DB 6; Length 1419;
 Best Local Similarity 57.2%; Pred. No. 2,4e-38;
 Matches 394; Conservative 0; Mismatches 289; Indels 6; Gaps 1;

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 436 GAGCTTAGAGCGGCCACCAATGCGCTTTGTGAAGGAATGTATCGGAAGGTGTTAC 495
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 1093 CGGCTTAACATGGAATGAGACCCGATTTGAAGATGCTTGTGATCTGCTTAAGACTT 1152
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 1453 AGCTTAGTGAAGTGGGACGACCACTTGT 1481
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 1096 AATCTAGTGAATGGCTTAATCAATGGT 1124
 |||||

RESULT 13
 ADN72798
 ID ADN72798 standard; cDNA, 1161 BP.
 XX
 AC ADN72798;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants Segid 693.
 XX
 KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
 KW growth regulator; animal feed product; thale cress;
 KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
 XX
 OS Arabidopsis thaliana.

XX
 EN WO2004035798-A2.
 XX
 XX 29-APR-2004.
 PD
 XX
 PF 20-OCT-2003; 2003WO-EP011658.
 XX
 XX 18-OCT-2002; 2002EP-00079408.
 XX
 XX (CROP-) CROPEDESIGN NV.
 XX
 PI Inze D, De Veylder L, Vlieghe K;
 XX
 DR WPI; 2004-348466/32.
 DR P-PSDB; ADN72799.
 XX
 PT Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX
 PS Claim 1; SEQ ID NO 693; 134pp; English.
 XX
 CC This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreduplication, biochemistry, signal
 CC transduction, storage lipid mobilization and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polynucleotide sequence is thale cress cDNA
 CC upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa
 CC transcription factor, given in an exemplification of the invention.
 XX
 SQ Sequence 1161 BP; 297 A; 216 C; 328 G; 320 T; 0 U; 0 Other;

Query Match 10.3%; Score 201.2; DB 12; Length 1161;
 Best Local Similarity 58.5%; Pred. No. 1.5e-37;
 Matches 372; Conservative 0; Mismatches 258; Indels 6; Gaps 1;

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 |||||
 736 GTCAAGCCGCTAAGTGGATTAACGTAATGTAATTAATTAATCTGGGATGCGCAAGATTG 795
 |||||

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Db	796	GGGATCTCAACGAGGCTTGAAGCAAAAGTTGTATCGGGAATTAATCAAGCAAT	855
QY	1213	ATATTGATAGATTTCAGATTGGAAGCTAAGGTGCTGATTTTGGTCTTGCATGAATTGCT	1272
Db	856	ATCTTACTTGATCGCCAAATGGAATGCAATGATTTCGAGTTTGGACTTGTAAGCTCTTG	915
QY	1273	TCTGATACAAACAGCAAGTATCAACACGATGATGGAACCTTTGGTACTTGGCTCG	1332
Db	916	GGGTCTGAGACAGTTATGTACTACTGTGTGATGGGAACCTTCGGTTAATGATACACA	975
QY	1333	GAATACGCTGAGAGGGAAGCTACGAGAAAGTCTGAAGCTTTTCTCATTTTGGCGTTGTG	1392
Db	976	GAATACGCTTGCACCGGAATGTAAACGAGAAGGTGATATCTAATAGCTTGGAACTACTA	1035
QY	1393	CTTTTGAGCTCATTTACTGACGTCGACCCGTTGAT	1428
Db	1036	ATCATGGAGATATATCATCGAAGAAACCCGGTTGAT	1071

RESULT 14

ABZ12561
ID ABZ12561 standard; DNA; 1950 BP.

Best Local Similarity 58.5%; Pred. No. 2e-37;
Matches 370; Conservative 0; Mismatches 260; Indels 3; Gaps 1.

OY	784	ACCTTCACATACGAGGAGCTAGAGTACGAGCCACCAATGGTTCTCCGAGGCGGAATGTTCTTA	844
Db	934	AATTTCAATATCTTAACAACATAGAGAAAGCCACAGGTTCTTTTGACAAACGGMAACAGCTT	993
OY	844	GGACAAAGCGGGGTTCCGGTTACGTGCACAAAGTGTTGCTAGTGGGAAAGAGTTGCT	903
Db	994	GGACAAAGCGGATTTTGGAACTGTCTTAATAAAGGGGGTTTCTTCACAGCGGAAGATATACGT	1053
OY	904	GTGAAGCAAGTTGAAAGTTGGGAGTGTGCAGGAGAGAGGAGTTTCAGGACAGAGTTGAG	963
Db	1054	GTGAAGCGGTTATTTCTTTAACACAGACATAGAGCAACCGATTTCTACATGAAGTCAAC	1113
OY	964	ATCATCAGCAGAGTTCACACAGGCACTGTGGTCTCTTGTGGTTAATTGCATGCCGCT	1023
Db	1114	ATGATCAGCACTGTGGAACATMAAACCTTTGTAAGTCTGCTGGTTGCAGTGTCTAGGA	1173
OY	1024	GCCAAAGAGTTGCTGTCTATAGTGTGTTGTTCTTACAAACAATCTCGAGCTTCACCTCCAT	1083
Db	1174	CCAGAGAGTCTCCTGTCTATGAAATACCTTCAGAAACAAGGACCTGTGATCATTCATCTTT	1233
OY	1084	GGCG---AGGAGCGGCTTACAATGGAATGGAGCCAGATTGGAAGATTGCTCTTGATCT	1140
Db	1234	GACGTGAACAGAGGAAAAACCTTGTAGCTGGCAGAGAAATACACGATCATCTTTGGAAAC	1293
OY	1141	GCTAAAGACTTTCTTAATCTTCAATGAAGATTGCATCTAAATCATTCACCGGTATATC	1200
Db	1294	GCTGAAGGATTTGGTATATCTGCATGACAGACAGTCGTGTGAAAATTTATTCACAGAGACATA	1353
OY	1201	AAGGCTTCAACATATTTGATATGATTTTCAAGTTGAGCTAAAGTGTCTGATTTTGGTCTT	1260
Db	1354	AAACCAAGATATATTTCTGCTAGATTCAAACTTCAACTAAAAACGCCGATTTTGGTCTG	1413
OY	1261	GCTAAGATTGCTTGTGATACAAACACCATATGATCAACAGTGTGATGGGAAACCTTTGGG	1320
Db	1414	GCGGATTCATTTCCAGAGCAGATMAAGCCATATTTAGCATCTGCCATTTGCAGGGAACCTTAGGT	1473
OY	1321	TACTTGGCTCCGGAATACGCTGCMAAGCGGAAAGCTCACGGAAGAGTCTGACGTTTCTCA	1380
Db	1474	TATATGGCTCCGAGAGTACTTAGCACATGTGTACAGTACAGAGATGATAGAGTTTACAGC	1533
OY	1381	TTTGGCGTTGGCTTTTGGAGCTCATTAATCGA	1413
Db	1534	TTTGGAGTTCTTGACTAGAGATTTGTAACATCGA	1566

RESULT 15

AA	C42860	
ID	AA	C42860 standard; DNA; 1353 BP.
XX		
AC	AA	C42860;
XX		
DT	17-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 37126.	
XX		
KW	Hybridisation assay; genetic mapping; gene expression control;	
KW	protein identification; signal transduction pathway; metabolic pathway;	
KW	promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-00301439.	
XX		
PR	25-FEB-1999; 99US-0121825P.	
PR	05-MAR-1999; 99US-0123180P.	
PR	09-MAR-1999; 99US-0123548P.	

PR 23-MAR-1999; 99US-0125788P.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
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; PRIOR APPLICATION NUMBER: US 60/159,122
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US-10-086-464-1

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Db 1141 GCTAAAGAGACTTCTTATCTTATGAAAGATTGCAATCTTAAATCATCTACCGTGAATC 1200
QY 1201 AAGGCTTCAAAACATATGATAGATTTTCAAGTTTAAAGTAAAGTTTGGATTTGGTCTT 1260
Db 1201 AAGGCTTCAAAACATATGATAGATTTTCAAGTTTAAAGTAAAGTTTGGATTTGGTCTT 1260
QY 1261 GCTAAGATTGCTTGTATACAAACAGCATGATCAACACGCTGTATGAGAGAACTTTGGG 1320
Db 1261 GCTAAGATTGCTTGTATACAAACAGCATGATCAACACGCTGTATGAGAGAACTTTGGG 1320
QY 1321 TACTGGCTCCGGAATACGCTGCAAGAGGAAAGCTCAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 TACTGGCTCCGGAATACGCTGCAAGAGGAAAGCTCAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 TTTGGCGTTGTGCTTTTGGAGCTCATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 TTTGGCGTTGTGCTTTTGGAGCTCATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 TATGTATATGACAGCTTATGTTGAGCTGGGACAGACATTTGCTTAAACGAGATCTGACAA 1500
Db 1441 TATGTATATGACAGCTTATGTTGAGCTGGGACAGACATTTGCTTAAACGAGATCTGACAA 1500
QY 1501 GGAGACTTTGAGGAGTTAGCTGATGCAAGATGAATGAATGAGTATGACAGAGAGAGATG 1560
Db 1501 GGAGACTTTGAGGAGTTAGCTGATGCAAGATGAATGAATGAGTATGACAGAGAGAGATG 1560
QY 1561 GGTGCAATGAGTCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 GGTGCAATGAGTCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 ATGAGCCAGATTTGGGTGCTTGAAGAGAAATGATCATCTGTGAGTCTTAAAGAGAGG 1680
Db 1621 ATGAGCCAGATTTGGGTGCTTGAAGAGAAATGATCATCTGTGAGTCTTAAAGAGAGG 1680
QY 1681 ATGAGCCAGATTTGGGTGCTTGAAGAGAAATGATCATCTGTGAGTCTTAAAGAGAGG 1740
Db 1681 ATGAGCCAGATTTGGGTGCTTGAAGAGAAATGATCATCTGTGAGTCTTAAAGAGAGG 1740
QY 1741 AGCAGTATCATATGAGAGATGAAGAGATTTAGAGAAATGACACTTGGAGCTCAAGAGTAC 1800
Db 1741 AGCAGTATCATATGAGAGATGAAGAGATTTAGAGAAATGACACTTGGAGCTCAAGAGTAC 1800
QY 1801 AAGGCCAGGAGTATGAGATATCCGACCATGATCTATGAGCTGTACCTGTCTGTTCA 1860
Db 1801 AAGGCCAGGAGTATGAGATATCCGACCATGATCTATGAGCTGTACCTGTCTGTTCA 1860
QY 1861 AGCAGAGAGGAGCCAAACCAACAGCGAAATGAGATGGGGAAGATTAAAGAGACCGGTGAG 1920
Db 1861 AGCAGAGAGGAGCCAAACCAACAGCGAAATGAGATGGGGAAGATTAAAGAGACCGGTGAG 1920
QY 1921 GGTATATGAGACCTTCTCTTTAA 1944
Db 1921 GGTATATGAGACCTTCTCTTTAA 1944
RESULT 2
US-10-086-464-3
; Sequence 3, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466

PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 60/159,122
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2189
TYPE: DNA
ORGANISM: Brassica napus
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(2189)
OTHER INFORMATION:
US-10-069-464-3

Query Match 100.0%; Score 1944; DB 13; Length 2189;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCCTCGAGCGGCTCTCGGAGGAGTGGTTCGCTCCATCTCCACCATCAAACTCCAGA 60
DB ATGTCCTCGAGCGGCTCTCGGAGGAGTGGTTCGCTCCATCTCCACCATCAAACTCCAGA 156
QY 61 ACCACCACTCTCTCTCCAGCTTCGCTCTCTCTCCACCAACACTTCTCTCTCCGCG 120
DB ACCACCACTCTCTCTCCAGCTTCGCTCTCTCTCCACCAACACTTCTCTCTCCGCG 216
QY 121 CCATCCACTATTCGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB CCATCCACTATTCGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276
QY 217 CCATCCACTATTCGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB CCATCCACTATTCGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 336
QY 241 CCGGCTCGAAGTACGCGCGGATCTCCACCGGACTTGTACTCTCTCTCTCTCTCTCT 300
DB CCGGCTCGAAGTACGCGCGGATCTCCACCGGACTTGTACTCTCTCTCTCTCTCTCT 396
QY 301 CCACCTTCACTCCAGAGACCAACGCTCCATCTCTCAAGGAGAGGATCTCTCGACT 360
DB CCACCTTCACTCCAGAGACCAACGCTCCATCTCTCAAGGAGAGGATCTCTCGACT 456
QY 397 CCACCTTCACTCCAGAGACCAACGCTCCATCTCTCAAGGAGAGGATCTCTCGACT 420
DB CCACCTTCACTCCAGAGACCAACGCTCCATCTCTCAAGGAGAGGATCTCTCGACT 516
QY 421 GGAATCGCATCGAGAGAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB GGAATCGCATCGAGAGAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576
QY 481 AAGAAGAAACGAG 540
DB AAGAAGAAACGAG 636
QY 541 GGTCCCAAGCGGAG 600
DB GGTCCCAAGCGGAG 696
QY 601 AACACACCGTCAGATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB AACACACCGTCAGATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 756
QY 661 CCAAGGCAACTCTCTCCACCTCCACCAACGCTCTCTCTCTCTCTCTCTCTCTCTCT 720
DB CCAAGGCAACTCTCTCCACCTCCACCAACGCTCTCTCTCTCTCTCTCTCTCTCTCT 816
QY 757 CCAAGGCAACTCTCTCCACCTCTCCACCAACGCTCTCTCTCTCTCTCTCTCTCTCT 816
DB CCAAGGCAACTCTCTCCACCTCTCCACCAACGCTCTCTCTCTCTCTCTCTCTCTCT 876
QY 817 TACTCGAGCGGTCT 840
DB TACTCGAGCGGTCT 840
QY 840 AGCACTTTCACTACGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840

DB AGCACTTTCACTACGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 936
QY 841 TTAGAGCAAGCGGAGT 900
DB TTAGAGCAAGCGGAGT 996
QY 901 GGTGTGAAGCACTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
DB GGTGTGAAGCACTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1056
QY 961 GAGATCATGAGAGAGATTCACCAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB GAGATCATGAGAGAGATTCACCAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1116
QY 1021 GGTGCCAAAAGATGT 1080
DB GGTGCCAAAAGATGT 1176
QY 1081 CATGGGAGGAGCGGCTCAATGGAATGAGACCAAGTGAAGTGTGTGTGTGTGTGT 1140
DB CATGGGAGGAGCGGCTCAATGGAATGAGACCAAGTGAAGTGTGTGTGTGTGTGT 1236
QY 1141 GCTAAAGCACTTCTATCTTCAATGAAGATTCATTAATCTTCAACGCTGTATTC 1200
DB GCTAAAGCACTTCTATCTTCAATGAAGATTCATTAATCTTCAACGCTGTATTC 1296
QY 1201 AAGCTTCAAAATATGATGATGATTCATTAATGATGATGATGATGATGATGATGAT 1260
DB AAGCTTCAAAATATGATGATGATTCATTAATGATGATGATGATGATGATGATGAT 1356
QY 1261 GCTAAGATGCTTCTATCAACACGCAATGATCAACAGTGTGTGTGTGTGTGTGTGT 1320
DB GCTAAGATGCTTCTATCAACACGCAATGATCAACAGTGTGTGTGTGTGTGTGTGT 1416
QY 1321 TACTGAGCTCCGAAATACGCTGCAAGCGGAAACCTCAACGAGAGTGTGACGTTTCTCA 1380
DB TACTGAGCTCCGAAATACGCTGCAAGCGGAAACCTCAACGAGAGTGTGACGTTTCTCA 1476
QY 1381 TTTGGGCTGT 1440
DB TTTGGGCTGT 1536
QY 1441 TATGTAGATGACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
DB TATGTAGATGACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1596
QY 1501 GGAACCTTTGAGGTTTGT 1560
DB GGAACCTTTGAGGTTTGT 1656
QY 1561 GCTGCAATGATGCTGT 1620
DB GCTGCAATGATGCTGT 1716
QY 1621 ATGAGCCAGATTTGT 1680
DB ATGAGCCAGATTTGT 1776
QY 1717 ATGAGCCAGATTTGT 1740
DB ATGAGCCAGATTTGT 1836
QY 1741 AGCAGTACATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB AGCAGTACATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1896
QY 1801 AAGCCAGAGGAGTACAGTATCCGACAGTATGATGATGATGATGATGATGATGATGAT 1860
DB AAGCCAGAGGAGTACAGTATCCGACAGTATGATGATGATGATGATGATGATGATGAT 1956
QY 1861 AGCAGCGAGGAGCAAAACCAACGCGAAATGAGATGAGGAGATTAAGAGAAACGGTCA 1920
DB AGCAGCGAGGAGCAAAACCAACGCGAAATGAGATGAGGAGATTAAGAGAAACGGTCA 1956
QY 1957 AGCAGCGAGGAGCAAAACCAACGCGAAATGAGATGAGGAGATTAAGAGAAACGGTCA 2016

QY 1921 GGTATATGAGACCTTCTTTAA 1944
Db 2017 GGTATATGAGACCTTCTTTAA 2040

RESULT 3

US-10-424-599-95479
; Sequence 95479, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 95479
; LENGTH: 2451
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_57229C.1
US-10-424-599-95479

Query Match 39.1%; Score 759.8; DB 16; Length 2451;
Best Local Similarity 65.0%; Pred. No. 8.7e-205;

Matches 1254; Conservative 0; Mismatches 627; Indels 48; Gaps 7;

QY 34 CCTCATCTCCACATCAAACTCCACACACACACTCTCTCCACACTTCCGCTCTCT 93
Db 246 CCCCTCCCTCCGCTGCAACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
QY 94 CCCACCAACCTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 153
Db 306 CCGGCGACACCTTCT 365
QY 154 TCTGCTCTACACCTTCT 213
Db 366 TCCGCTCTCCACCT 425
QY 214 CCACCT 273
Db 426 TCAACTTGGCGCCATCGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 485
QY 274 CCGTCT 333
Db 486 CCGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 545
QY 334 TCACCGAAGAGAGATCT 393
Db 546 CCGTCCGATCGAGA-----CCGACCACTCGGTGCTCTCTCTCTCTCTCTCTCTCT 593
QY 394 GACGTTATCAACAGAGT 453
Db 594 TCGAGTATTTGACCGGT 653
QY 454 ATAGTGAATCTGATTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 513
Db 654 GTGTGACATTTCTGTGATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 713
QY 514 TACTATGTTCTCCGCACT 573
Db 714 TATGTCGCGCGCGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 773
QY 574 CAGCAACATGCGCGCAACAAACCGCAACACCGCTGATGATGATGATGATGATGATG 633
Db 774 CGTCAA-----TGGCAACAGATGTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 827

QY 634 CCAACACCACTTAAGGCTCCATCTCCACGAG-----CACTCTCTCTCTCTCTCTCT 684
Db 828 CTTCCAAAGCCATCGCACCACTGCTCCACCGCTTATGCTGCTCAACTCTCCCAACCA 887
QY 685 CCAACGCTTTTCAATGACGACGAGCGGCGCTCCG-----ACTACTGAGACCGTCCAGTT 738
Db 888 CCGCTCTCTTTCAATGACGACGAGCGGCGCTGATGATGATGATGATGATGATGATGAT 947
QY 739 CTTCTCTCCACCGCTCTGAGGCTTTGTTAGCTTTCTCCAAAGCACTTTCAATGAG 798
Db 948 CTTCT 1007
QY 799 GAGCTAGTAGACCCCAATGCTTCTCTGAGCGCACTTTGATGACAAAGCGGCTTC 858
Db 1008 GATTTGGACGCGCACTGATGCTTCTGATGCACTCTCTTGGACAGGAGATTT 1067
QY 859 GGTACGTGCAAAAGGTGTGTGCTTCTGAGGAAAGATTTCTGAGAGCTTTGAA 918
Db 1068 GGTATGTCACAGAGAAATTTCTCCAAAGCGCAAGAGTGCATGAGCAATTTGAG 1127
QY 919 GTTGGAGTGTGACGAGGAGAGAGAGGTTTCAGGACGAGTTGATCATCAGCAGATT 978
Db 1128 GTTGAAGCGGCGCAAGGAGCGTGAATTCAGGCTGAAGTTGAGATTAATGCTGTTC 1187
QY 979 CACACAGGCAATCTGCTCTCTGTTGTTATGATGCGCGGTCCAAAGATTTGCTT 1038
Db 1188 CATTCAACAGCTTTCTTTCTTTGTTGATGATGATGATGATGATGATGATGATGATGAT 1247
QY 1039 GTCTATGAGTTGTTCTTCAACAAATCTGAGCTTCACTCTCCATGCGAGGAGCGACT 1098
Db 1248 GTTATGATTTGTTCTTCAACAAACATTTGAATTCATTTGATGATGATGATGATGAT 1307
QY 1099 ACAATGATGAGAGACCGAGTGAAGATTTGCTTTGATGCTGCTTAAGATTTCTTAT 1158
Db 1308 ACCATGATGAGCCCAAGAGCTGAAGATTTGATGATGATGATGATGATGATGATGAT 1367
QY 1159 CTTCAATGAAGTTGCAATCTTAAATTCATTCACCGGATATCAAGGCTTCAAAATATG 1218
Db 1368 CTTCAATGAAGTTGCTATCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1427
QY 1219 ATGATTTCAAGTTGAAGTGAAGTTGCTGATTTGCTGCTTAAGATTTCTTGTAT 1278
Db 1428 CTGATTTTAAGTTGAAGCAAGTTGCTGATTTGCTGCTTAAGATTTCTTGTAT 1487
QY 1279 ACAAACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
Db 1488 GTCAATACCATGTTTCTACTGAGTGAAGGAGCTTTGGGTATTTGGCTCCAGAAATAT 1547
QY 1339 GCTGCAAGCGAAGCTCAGAGAGAGTCTGAGTTTCTCATTTGGCGTTGCTTTG 1398
Db 1548 GCTTCTAGTGAAGAACTGACAGCAAAATCAGATGTTTCTCTATGAGATCATGCTCTTC 1607
QY 1399 GAGCTCATTTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1458
Db 1608 GAGTTAATACCGGAGCGAGCGGCTGATTAATAATCAAACTTTCATGAGAGATGTTG 1667
QY 1459 GTTGAATGAGGAGCACTGTTTAAAGGACATGAGCAAGAGCACTTTAAGGTTTA 1518
Db 1668 GTAGCTGAGGCTTGTGCTTGTCTACAGAGTTTGGAGAGAGATTTTATTTCTAT 1727
QY 1519 GCTGATGCAAGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1578
Db 1728 ATTAGCCCAAGGCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1787
QY 1579 GCTGCGGCTTTGTTGCTCAATTCAGCTGCGGAGACTTCGATGAGCCAGATTTGCGT 1638
Db 1788 GCTGCGGCTTTGCTCAATTCAGCTGCGGAGAGGCTGACCAAGATGAGCCAGGTTTGC 1847
QY 1639 GCGTTAAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1698
Db 1848 GCTCTGAGAGAGATGTTCTTCTAGCAGATCTTAAAGAGAAATTTAGCTGGAACAGC 1907
QY 1699 AATGATTAAGCTCATAGAGAGAGCAAGATTAATGATGATGATGATGATGATGATGAT 1758

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Db      1908 ACATATGACGTTCTCA---TGAAGCTCAGATTATGACACTGCACAGTACCAAGGAGAGC 1964
QY      1759 ATGAGAGAGTTTGGAAAAATGGGACCTTGGAACTCGAGAGTACCAAGCGGCTGAGTAC 1818
Db      1965 ATGAAAAAGTTTCAGAAAAATGGGACTTGGGAATCTCAGAGATGATGGTGAACAGAGTAC 2024
QY      1819 AGTATCCGACCAAGTGCATGAGTGTACCTGCTGCTTCAAGCAGCGAGG-----1870
Db      2025 AGTCCGCTTCAAGTGTGATGTTTAAACCATCAGGCTCAGTATGATGAGCAGAGC 2084
QY      1871 -GCCAAACCAACGCGGAAATGAGATGGGAGATTAAAGAAACCGTCAAGGTTATAGT 1929
Db      2085 CGCCAAACCAACAGGGAATGGAATGAAAGATGAAG---AACATCAAGGTTTCAGT 2141
QY      1930 GGAACCTTCT 1938
Db      2142 GGAAGTTCT 2150

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RESULT 4

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US-10-425-114-9117
; Sequence 9117, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OR INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9117
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700833950_FLI
US-10-425-114-9117

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Query Match      33.0%; Score 642.2; DB 16; Length 1424;
Best Local Similarity 71.2%; Pred. No. 1.8e-171;
Matches 912; Conservative 0; Mismatches 348; Indels 21; Gaps 4;

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QY      673 CCTCACCTCCACACCGGCTTTTCATGAGCAGCAGCGGCGCTCCG-----ACTACTCG 726
Db      9   CCTCCCCACACCGGCTTTCTTTTCATCAGACAGAGGCGGATCTGATCAACAATTCA 68
QY      727 GACCGTCCAGTTCTTCTCCACCGTCTCCAGGCGTTGTAGGCTTCTCCAAAAGCACT 786
Db      69 GGGGGGAAATTTCTTCTCTCTCTCTCCAGAAATTCATTGGGGTTCTCTTAAGAGACA 128
QY      787 TTCACTACGAGAGAGCTAGTACAGCCAAATGTTTCTCCAGGCGAACTTTGTAGGA 846
Db      129 TTCACTATGAGAGAGTTGGCAGCGCACTGATGGCTTCTGTATCCAACTCTCTTGA 188
QY      847 CAAGGGGGTGGTTACGTACGACCAAAAGGTGTGCTTCTAGTGGAAAAGAGTTGCTGTG 906
Db      189 CAAGGAGAGATTGGATATGTGCAAGAGAAATCTTCCCAAGCGCAAGAGAGTGGCAGTG 248
QY      907 AAGCACTTGAAGTTGGAGTGTGTGACGAGAGAGAGGAGTTTCAAGCAAGGTTGATC 966
Db      249 AAGCAATTGAAGCTGGAAGCGGCAAGGGAGCGTGAATTCGAAGCTGAAGTTGAGATA 308
QY      967 ATAGAGAGAGTTACCAACAGGAGCTTGTGTCTCTTGTGGTATGCACTGCGCGGTGCC 1026
Db      309 ATTAGCGGTGTCCATCACAAGAGCTTTGTTTCTTGTGATGATGCACTGCGGTCC 368

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QY      1027 AAAAGATGCTTGTCTATGAGTTTGTCTTAACAACAATCTCGAGCTTCACTCATGCG 1086
Db      369 CAGAGGCTCTGTTTATGAAATTTGTTCCCAACAACAATGGAATTCATTGCAATGGA 428
QY      1087 GAGGAGCGGCTTCAATGAAATGAGACACAGATTGAAGTTCTCTTGGATCTGCTAAA 1146
Db      429 AAGGAGAGACTTCCATGATTTGGCCCAAGACTAAAGATTCTTAGATCTGCTAAG 488
QY      1147 GACCTTCTTATCTCATGAGATTTGCAATCTTAAATCATTTACCGTGTATCAAGGCT 1206
Db      489 GACCTGCGTATCTTCAATGAAAGTTGTCATCTTAAATCATTCATCGTATCAAAATCT 548
QY      1207 TCAAACTATGATTAATTTCAAGTTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 1266
Db      549 GCCAACAATCTTCTGATTTTAAAGTTGAAGCAAAAGTTGCAAGTTTGTCTTGAAG 608
QY      1267 ATTGCTTCTGATTAACAACGCACTGATCAACAGTGTGATGGGAACTTTGGTACTTG 1326
Db      609 TTTTCTTCTATGTCATTAACCATGTTTCTACTGAGTGAATGGGAACTTTGGGTATTTG 668
QY      1327 GCTCCGGAATACGCTGCAAGCGGAAAGCTTCAAGGAAAGTGTACGTTTCTCATTTGGC 1386
Db      669 GCTCCAGATATAGCTTCTAGTGAAACTCAGACAAATCAGATGTTTTCTCTATGGA 728
QY      1387 GTTGTGCTTTTGGAGCTCATTTACGAGCTGCAAGCTGATGCCCAACAATGCTATGTA 1446
Db      729 ATCATGCTCTTGTGATTAATTAACGAGAGCGCAGGTTGATTAATACTTAACATG 788
QY      1447 GATGACAGCTTAGTTGACTGCGGACCACTTGTCTTAACGAGATCTGACAAAGAGAC 1506
Db      789 GAGATAGTTTGTGATGATTTGGGCTTAGGCTTTGCTCAGCAGGCTTTGGAAGAGATAT 848
QY      1507 TTTGAGGTTTATGCTGATGCAAGATGATATATGCTATGCAAGAGAAATGGCTGCG 1566
Db      849 TTTGATCTATTAATGACCCAGGCTCCAGATATGATGATCTCTAGAGATGCGACAG 908
QY      1567 ATGTTGTTTGTGCTGCGGCTTGTGTCATTCAGCTGCGCGGACCTCGCATGAGC 1626
Db      909 ATGTGCTTCTGCTGCGGCTTGTGTCATTCAGCTGCGGACCTCGCATGAGC 968
QY      1627 CAGATTGCTGCTGCTTGAAGAAATGATATCTGATGATCTTAACGAAAGATGAGA 1686
Db      969 CAGGTTTCCGCGCTCTGAAAGAGATGCTCTCTAGCAGATCTGAATGAAGAAATAGA 1028
QY      1687 CCAAGTCAAGCAATGATATCACTCTATACGAGAGAAACCAAGGATTAAGCTCGAGCC 1746
Db      1029 CTTGACACAGCACTATGATATGTTCTCA---TGAAGCTCAGATTATGACACTGCACAG 1085
QY      1747 TACATGAAAGCATGAAGAGTTTGAAGAAATGCACTTGAATCAAGAGTACAAAGCC 1806
Db      1086 TACAAGGAAGACATGAATAAAGTTTCAAGAAATGCAATTTGGAACTCAGAGATATGCTGA 1145
QY      1807 ACGGCTGATCAGTATATCCGACAGTGAATGAGACTGTAACCTGCTGCTTCAAGCAGC 1866
Db      1146 AGCAGTGAATAGTACGCGCTTCAAGTATGATGTTTAAACCATCAAGGCTCAAGTAT 1205
QY      1867 GAGG-----GCCAAACCAACGCGCAATATGAGATGGGAAAGTTTAAGAAACCGGT 1917
Db      1206 GAAGCAGAGAGCGCCAAACCAAGGGAATGAAATGAAAGATGAAG---AACAAAT 1262
QY      1918 CAGGTTATATGAGCACTTCT 1938
Db      1263 CAAGGTTTCAGTGAAGTTCT 1283

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RESULT 5

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US-10-437-963-59942/C
; Sequence 59942, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```

```

1  APPLICANT: Cao, Yongwei
2  APPLICANT: Wu, Wei
3  APPLICANT: Boukharov, Andrey A.
4  APPLICANT: Barbazuk, Brad
5  APPLICANT: Li, Ping
6  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
7  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
8  FILE REFERENCE: 38-21 (53221)B
9  CURRENT APPLICATION NUMBER: US/10/437,963
10 CURRENT FILING DATE: 2003-05-14
11 NUMBER OF SEQ ID NOS: 204966
12 SEQ ID NO 59942
13 LENGTH: 1896
14 TYPE: DNA
15 ORGANISM: Oryza sativa
16 FEATURE:
17 OTHER INFORMATION: Clone ID: PAT_MRT4530_61518C.1
18 US-10-437-963-59942

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Query Match	32.9%	Score 640;	DB 17;	Length 1896;
Best Local Similarity	68.4%	Pred NC 8	7e-171.	

QY	548	CAAAGCCGAGAGCCTTACGCTGGACAGAGCAACAATGGCGCAACAAACGCAACACC	605
Db	1800	CAAGGAGGATGGCATATGTGTGATCATACCAAGAAAGTTGGACGCAAAAATGCCCAACACC	1744
QY	606	ACCGTCAGATCAATGTCGTGACGTCACTACCAACCACCTTAAGGC---TCATCTCCACC	662
Db	1740	TCGGCTGGACATGTATGTAAATGACCCATCACCTCCGGCAGGGATGCAAAACGTCCTC	1681
QY	663	ACGGCACTCTCTCCACCTCCACCAACCGGCTTCAATGAGACACACGGCGGCTCCGAC--	720
Db	1680	TCACACAGCCACCATGACCCCTCCAGCTCTATGTATTAACACACACACGGGTCTGGGCTC	1621
QY	721	-TACTCGAACCGTCCAGTTCTTCTCTCCACCGTCTCAGGGCTTGTGTTAGGCTTCCAA	779
Db	1620	TTACTCAGGTGAGAGATCCTTACCAACACCATCCCTGGCGGTGCCCTTGGTTTCTCAAA	1561
QY	780	AAGCACTTTCANATACGAGAGCTTAGTAAAGCCAAATGGTTTCTCCAGCGCACTT	839
Db	1560	GAGCACTTTATCTTATGAAAGACTGTTAAGGGCAACGATGGATTCTCTGATGCTAACT	1501
QY	840	GTTAGGACAAAGCCGGGTTGCGTTACGTGCACAAAGGTGTGTTGCTAGTGGAAAGAACT	899
Db	1500	CCTTGGACAAAGGTGGTTTGGCTATGTCCATAGAGAGTGGCTGCTCTATCGAAAAAGCAT	1441
QY	900	TGCTGTGAAGCAGTTGAAGTTGGAGAGTGTCAAGGACAGAGGGAGTTTCAGGACAGAGT	959
Db	1440	TGCTGCGAAACATTTGAAAGTTCTTAGTGGCGAAGTAAAGGTGATATCCAGCGGAGGT	1381
QY	960	TGAGATCATACGACAGATTCAACCAAGGCATCTGGTGTCTCTGTGTTGGTTATTCATCGC	1019
Db	1380	TGAGATTTATCAGCAGAGTACATCAACAAACATCTGTCCTCAATGGGTGGTTATTCATTTCC	1321
QY	1020	CGGTGCCAAAGATTTGCTGTGTCTATAGATTTGTTCTCTAACAAACATTCGAGCTTCACT	1079
Db	1320	TGGGGGCAAGAGATTTGCTGTGTATGTATGTGTGCTCCCAACAAACATTTGAATTCACCTT	1261
QY	1080	CCATGCGCAGAGGACGGGCTCAATAGGAAATGAGACACAGATTGAAGATGTGCTTGGATC	1139
Db	1260	GCACGGAAAGAGCCGACCAACATATGAGGTGGCCCAAGACATTAAGATTTGTTGGAGGC	1201
QY	1140	TGCTAAAGACCTTTCTTATCTTCAATGAAGATTTGCATCTCTAAATTCATTCACCGTGATAT	1199
Db	1200	TGCAAAAGGTTTACCTTATCTTCAATGAAGCTGCACTTAAGTATCATTCATCTGATATAT	1141
QY	1200	CAAGGCTTCAAACTATTTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCT	1259
Db	1140	TAAAGGCTCAAAACATCTCTTGTGATTTTAAATTGATCTTAAAGTTGCTGATTTTGGACT	1081
QY	1260	TGCTAAAGATTGCTTCTGATACAAACAGCATGATATCAACGCTGTGATGGAAACCTTTGG	1319

Dp	1080	TGCTAAGTTCAACAGCTGATTAATTAACCTCAATGTTTCGACAAAGAGTAATGGCACATT	793
Qy	1320	GTACTTGGCTCCGGAAATACGCTGCACAGCGGAAAGCTCACAGAGAAAGTCTGACGTTTTCTC	1379
Dp	1020	AATATTCACCAACAGATACCGCATCTTCTGGCAAGCTCACTGAAATCAATGTCTTCTC	961
Qy	1380	ATTGGAGCTTGAGCTTTGGAGCTCACTTACGTGAGCTGAGCCGTTGATGCGAACAAATGT	1439
Dp	960	CTATGGAGTTATGCTTTCTTGAGTTTAATTAACCTGGCTGCGCAATGTATTCMAATCAAC	901
Qy	1440	CTATGTAGTACACAGCTTAACTTGACTGGGACGACCAATGCTTTAACGAGCATCTGAC	1499
Dp	900	ATATATGATGACACAGCTTGGTTGACTGGGCAAGGCCCTTTACTGATGCAACGCTTGAGAA	841
Qy	1500	AGGAGACTTTGAGGCTTTAGCTGATGCAAAGATGCAATATGTGGTATGACAGAGAGAT	1559
Dp	840	TGGTAACCTACAGAGAGTTAGTAAGATCCTCGGCTTGGCAAGATTTTCAATCCCATGAGAT	781
Qy	1560	GAGTCGCATGTTGCTTGTGCTGCGGCTGTGGTTGGCTTGGCATTCGACGTGCGGACACTCG	1619
Dp	780	GGCGAGATGATTGCTTGTGCAAGTGCATGTGTAACGCATTTCCGCTGTGTGCGCCACG	721
Qy	1620	CATGAGCCAGATTGTGCGTGGCTTTGAGAGAAATGTATCACTGTCAATCTTAAACGAAG	1679
Dp	720	CATAGGCGAAGTTGTCCGGGCTTTGGAAAGGTGACGTGTCTTGAAGGATCTTAAAGAAAG	661
Qy	1680	GATGAGACCAGGTCAAAAGCAATGTAATACACTGATACCGAGAGAAAGCACCGATTAATGAC	1739
Dp	660	TGTTCCGCTGTGTACACGCCGCTAATTTTGGATGTAC--AGAGCTCTGCATATATATTC	604
Qy	1740	GAGCCAGTACATATGAACATGTGAAGAAATTTAGAGAAATGGCACTTGGAACTCAAGAGTA	1799
Dp	603	TGGCAATATCAACGAGAGCATGAAAGAAATTCAGAGAAATGGCTTTT--ACCAACAATAA	547
Qy	1800	CAAGGCCACGGGTGAGTACAGTAAATCCGACCAATGACTATGACTTTAACCCGTTGCTTC	1859
Dp	546	TGATACGAGCATCAATACAGCCGACCAACCAACGAGTATGGCAATACCCCTTGCATC	487
Qy	1860	AAGCAGGAGAGGCGCAAAACGACGCGCAAAATGAGATGGGAAAGATTTAAGAAACGGTCA	1919
Dp	486	AAGCAGGAGAGGCGCAAAACCAAGGAATGCAAGACAGAGCAACCAAGAGAGGCGGCTA	427
Qy	1920	GGGT 1923	
Dp	426	CAGT 423	

```

RESULT 6
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
; LENGTH: 1724
;
; TYPE: DNA
;
; ORGANISM: Zea mays
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326

Query Match          32.1%; Score 624.6; DB 16; Length 1724;

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Best Local Similarity 65.5%; Pred. No. 2e-166;
Matches 1001; Conservative 0; Mismatches 504; Indels 24; Gaps 5.

Qy	475	CTCTGT---AGAGAAAGCAGCGGAGACGAGAAAGATGCTTACTATGTTCTCCGCCA	531
Db	61	TGCTGTCTCCGAAAGAGCGCGCGCGCGCGCGCTCAGACACTAGGATATCCG	120
Qy	532	CTCTCTCTGCTGCCAAAGCCGAGGACTTACGGTGGACACGACGACCAATAGCGGGAA	591
Db	121	CCGCCCCCGCGCGGTACAAAGGAGATTCATACGGTGGAAAGTACCAAGTTGGAGAA	180
Qy	592	CA---AAAGCAACACACCGGTGATGATGTCGTA-----CGTCACTACCA	639
Db	181	AAAGCGCTCTCTGCTCCACCCCTGGAACATGAGTAAATGACACCCCTTGCTCCGCA	240
Qy	640	CCACTAAGGCTCCATCTCCACCACCGGCAACTCTCTCCACTCCACACCGCTTTCATG	699
Db	241	GCATATGCCATAGTCTCTCCAGACCGCCAGCGCCGCAACACAGCGATGCTAAATAGT	300
Qy	700	AGCAGCAGCGCGGCTCCGACTACTGGAACCGTCCAGTTCTTCTCCACCGCTCCAGGG	759
Db	301	AGTGTGGATCTGGTTCATATTACTCTGGTGGAGATCTTACCTCCACATCTCCCTGAT	360
Qy	760	CTTGTGTAGGCTTCTCCAAAGACCTTTCACATAGCAGGAGGTACTAGACCCACAT	819
Db	361	GCTGTCTCTGCTCTCGAAGAGACCTTACTACGAAAGTTGTGAGGCTACTGAT	420
Qy	820	GATTCTCCAGGCGAACTTGTAAGCAAGCGGGTTCGGTTAGTGCACAAAGGTGTG	879
Db	421	GGATTCTCGATGCTATATCTCTTGACAGAGTGGTGGTATGTTACAGAGGATTG	480
Qy	880	TTGCTTATGGGAAAGAAATTGCTGTAGACAGTTGAAACTTGGAGTGGTCAAGGAG	939
Db	481	CTGCCTAATGCAAGAGATTCGTAAAACTGAACTGGAAGTGGCCAGGCGAG	540
Qy	940	AGGAGTTTCAGGAGAGGTTGATCATGACAGAGTTCAACACAGGCACTCTGATCT	999
Db	541	CGTAGTTCAGGCTGAGGTTGAAATTAACGCCAGATACATACAAACACTTGTGTCT	600
Qy	1000	CTTGTGTGTTATTCATGCGCGGTGCCAAAGATTTGCTTCTATGATGTTTCTCTAAC	1059
Db	601	TTGTGTGCTATTCATGATTTCTGAGGCAAGGCTGCTGTCTATGATGTTTGTCCCAAT	660
Qy	1060	AACAATCTGAGCTTCACTTCATGCGAGGGAAGGCTTCAATNGAAATGAGACACAGA	1119
Db	661	AAACATTTGAAATTCACCTTACATGCGAAAGTGAACCAACAAATGGAGTGGCTGTAGA	720
Qy	1120	TTGAAGATTTGCTTGGATTCGCTAAAGACTTTCTTATCTTCAATGAAGATTGCAATCT	1179
Db	721	TTAAAGATGATTTGGGTGCTGCCAAGGTTTAGCTTATCTTCAATGAAGCTGCATCCA	780
Qy	1180	AAATCATTCACCGTGAATCAAGGCTTCAACAATTTGATGATTTCAAGTTGAAGCT	1239
Db	781	AGATCATTCACGTGACATAAAGCATCTAACATTTCTTGACTTCCATTTGAAGCT	840
Qy	1240	AAGTTGCTGATTTTGTCTTCTAAGATTGCTTGTATTAACAACGCACTGATATCA	1299
Db	841	AAGTTGCTGATTTTGTGCTTGCAAAGTTCACTTCACTGATTAACAACACCAATGTTTCAGA	900
Qy	1300	CGTGTGATGGAAACCTTGGGACTTGGCTCGGAATACGCTGCMAAGCGAAAGCTCAGC	1359
Db	901	AAGTATATGGGCACTTTGGTATTTTGGCACTGATGATCTTTCGGCAAGTATACA	960
Qy	1360	GAGAAATCTGAGCTTTCTCATTTGGCGTTGTGCTTTTGAAGCTCATTACTGACGTGCA	1419
Db	961	GAAAAATCTGATGATTTTCTTCGGAAGTCATGCTTCTGAGCTTATTACTGGGCGGGCA	1020
Qy	1420	CCGTTGATGCCAACATGTCTATGTAGATGACAGTTAGTTGACTGGGCAAGCAATTG	1479

Db	1021	CCAGTTGACACCAACCCAAATATATATGATGACAGACGTTGGTTGACTCGGACAAAGCCATTA	1080
Qy	1480	CTTAAACCGACATCTGAGCAAGAGACTTTGAGGGTTTACGTGATGCAAAATGAATAT	1539
Db	1081	CTGATGCGACACTCTTGAGGATGGGAAATATGATCTTTAGTGATCCTCGGCTGGAAAG	1140
Qy	1540	GGGATATACAGAGAGGAGATGGCTCGATGATTCCTGTGCTGGGCTTGTGTTGGCCAT	1599
Db	1141	GACTTCATCTTAATGAGATGGCAAAATATATACCTGTGACGCTGATGHTGACGCAT	1200
Qy	1600	TCAGCTCGCGCAGACCTCGCATGAGCCGATTTGTGGTGGGTTAGAAAGAAATGTAACA	1655
Db	1201	TCTGCAGCTCGTCCGCCACCATATAGTCAGGTTGTTGGGCTTTGGAGGAGCAATGTGCT	1266
Qy	1660	CTGTCCAGATCTTAAACGAAAGGATGAGACAGGTCAAAAGCAATGTATACGCTCATACGGA	1712
Db	1261	TTGGAGAGCCTTAAATGAAGTGTGTTGGCTGGCCATATGCCCTCTTTTGGGTCAATAC---	1317
Qy	1720	GGAAACACCGATTTATGACTTCGAGCCAGTACATGAAAGCATGAAGAAATTTTAGGAAATG	1779
Db	1318	AGCAGCTCCGATTTCAGATTCTGGCCAGTACAAACGAGCATGAAAGAAATTTCAAGAAATG	1377
Qy	1780	GCACATTGGAATCTCAAGAGTATACAAAGCCACGGGTGATACAGTAATCCACACAGTGACTAT	1835
Db	1378	GCATT-----CAACAACATCTATACAGAGCCATATACAGGCGCCAACACAGTGAATAT	1431
Qy	1840	GGACTGTACCCGCTGTGTTTCAAGCAGCGAGGGCCAAACCAACGCGAAATGGAGATGGGG	1895
Db	1432	GGACAGATATCCCTCTGCATCAAGCAGCAGAGGGCCACACAGACGACAGAAATGAGTGGGT	1491
Qy	1900	AGATTTAAGAAACCGATCAGGGTATATAG	1928
Db	1492	GCATATGAACAAAGTGCTACAGTGGTGG	1520

```

RESULT 7
US-10-425-115-57011
; Sequence: 57011, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Placis
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 57011
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_151984C.1
US-10-425-115-57011

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Query Match	32.0%	Score 621.2	DB 18	Length 2886
Best Local Similarity	67.1%	Pred. No.2.4e-153		
Matches 948	Conservative 0	Mismatches 443	Indels 21	Gaps 4
QY	529	CCACCTCTCTCTGTGCCCAAGACCGGAGACCTTACGGTGGACAGACGAAACAATATGGCGG	588	
Db	1172	CCGCGCGCCCCAGGTCGCTACAGGAGGATCCATTAAGGTGGACGTGCAAGAATGGTGGCG	1231	
QY	589	CACA- --AAAGCACAACCAACCGTCAGATCATGTCTGA-----GTCATCTACA	636	
Db	1232	CAAAATGGCGCTCTCTGTCCACCCCTCAAAATGGTGAAGTGCACCTTGGCTTCG	1291	
QY	637	CCACGACCTAAGGCGTCATTTCCACACGGCAACCTCTCCACCTCCACGACCGCTTTC	696	
Db	1292	CCAGGAGATTCCATATGATCTTCCAAACAGGCCAGCGCCGACACACGAGCATGTAAAT	1351	

QY	1033	TTGCTTGTCATAGAGTTTGTTCCTTAACAACAATCTGAGCTTCACTCCATGGCCGAGGGA	1092
Db	1738	CTGCTGTCTAATAGATTGTGCCCAATPAACAATGGAAATTCACCTACCTGCGAAAGGT	1797
QY	1093	CGGCGTCATGGATGGAGCAGACAGATTGAAGATTCTTCTGGATCTGCTAAAGACTT	1152
Db	1798	CGACCAACAAATGGAGTGGCCTGCTAGATTAAATCAAGTTTGGGTGTGCGAAGGTTTA	1857
QY	1153	TCTTAATCTTCATGAAAGATTGCAATCCTAAATCATTCACCGTGATATCAAGGCTTCAAC	1212
Db	1858	GCTTAATCTTCATGAAAGACTGCCATCCAAAGATCATTCATGTCATMAAGGATCTAAC	1917
QY	1213	ATATGATTAATTTCAAGTTTGAAGCTPAAGGTGCTGATTTTGGTCTTGGTAAGATTGCT	1272
Db	1918	ATTCTTCTTGACTTCCAAATTTGAAGCTPAAGGTGCTGATTTTGGTCTTGGTAAGATTGCT	1977
QY	1273	TCTGATCAAAACAACGCACTGATCAACAACGTTGTATGGAAACTTTGGGTACTTGGCTCG	1332
Db	1978	ACTATATAACAACACCACTGTTTGCACAAGATATGGGCACTTTGGGTATTGGCACCT	2037
QY	1333	GAATACGCTGCAGCGGAAAGCTCAACGGAAGAATCTGACGTTTCTCATTTTGGGTTGTG	1392
Db	2038	GAGATGATCTTCTTGCGCAAGCTAAACGAAAAATCCATGATTTTCTTCCGAGGTATG	2097
QY	1393	CTTTTGAGGCTCATTCCTGACGCTCGAACCCGTTGATGCAACATGTCTATGTGATGAC	1452
Db	2098	CTTCTTGAGCTTATTAACGCGCGGACAGCTTACACACCAAACATATATGATGAC	2157
QY	1453	AGCTTAGTGACTGCGGCGACGACCAATGCTTAACCGAGATCTGACAGAGACTTGA	1512
Db	2158	AGCTTGTTGTACTGGGCAAGGCCATTTACTGATGCGAGCACTTGAGAGATGGGAATTAGAT	2217
QY	1513	GCTTTAGCTGATGCAAAAGATGAAATATATGGGTATGACAGAGAGATTCGCTCGATGGTT	1572
Db	2218	GCTTTAGTGAATCCCTCGGCTGGAAAGACTTCAATCTTAATGAGATGGCAAGATGATA	2277
QY	1573	GCTTGATGCGGGGCTTGTTGCTCGACATTCAGCTGCGCGCAACCTCGCATAGGCAGATT	1632
Db	2278	GCTTTGACGCTGCAATGTGTAGCGCATTTCTGCACTCGTCGCGACAGTATAGTCAAGTTC	2337
QY	1633	GTGCGTGGCTTAGAAGAAATGTATCACTGTCAAGTCTTTAAAGAAAGGATGAGACAGCT	1692
Db	2338	GTCGGGCTTTGAGAGGCAATGTGCTTTGGAGGACCTTAAATGAAGGTGTTGCGCTTGGC	2397
QY	1693	CAAAAGCATGTATACAGCTCATACGGAAGAAAGCAACGATTATGATCGAGCGCAGTAAAT	1752
Db	2398	CATACCCGCTTTCTTTGGCTCAATC---AGCACTCTCGATTACGATTTCTGGGCCATGTAAC	2452
QY	1753	GAAGACATGAAGAAGTTTAGAAAAATGGCACTTGAACTCAAGAGTACAAACGCCACGGGT	1812
Db	2455	GAGGACATGAAGAAGTCAAGAAGATGGCATTT-----CAACAACAATATCCGACAGC	2508
QY	1813	GAGTACAGTAATCCGACCACTGATCTATGSACTGTACCCGTCTGGTTCAAGACGCGAGGGC	1877
Db	2509	CAATACAGCGCGCCCAACCGTAAATATGACAGATACCTCTGCAATCAAGCGCAGAGGCG	2566
QY	1873	CAAAACACACGGAAATGGAGATGGGGAAGATTAAAGAACCCGCTCAGGGTATATAG	1928
Db	2569	CACCAACCGCAGAGATGAGTGTGGGTGCAAATGAGAAAGGTGTACAGTGTGTG	2624
RESULT 9			
US-10-425-114-33031			
/ Sequence 33031, Application US/10425114			
/ Publication No. US20040034888A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Liu, Jingtong			
/ APPLICANT: Zhou, Yihua			
/ APPLICANT: Kovalic, David K.			
/ APPLICANT: Screen, Steven E			
/ APPLICANT: Tabaska, Jack E			
/ APPLICANT: Cao, Yongwei			

	TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
	FILE REFERENCE: 38-21(53313)B
	CURRENT APPLICATION NUMBER: US/10/425,114
	CURRENT FILING DATE: 2003-04-28
	NUMBER OF SEQ ID NOS: 73128
	SEQ ID NO 33031
	LENGTH: 2881
	ORGANISM: Zea mays
	FEATURE:
	OTHER INFORMATION: Clone ID: UC-ZMFLMO17055B12_FLI
	US-10-425-114-33031
Query Match	31.9%; Score 619.6; DB 16; Length 2881;
Best Local Similarity	66.7%; Pred. No. 6,8e-165;
Matches	918; Conservative 0; Mismatches 449; Indels 9; Gaps 2;
Qy	553 GGAGGACCTTACGTTGAGCAGCAGCAATGCGGCAACAAACGAAACACACCCCTCA 612
Db	1259 GGTGGAAAGTACAGAGTTGGCAGCAAAATGCGCCTCTGCTCACCCCTGAACATGTG 1318
Qy	613 GATCATGTCTGACGCTACCAACACCACTTAAGGCTCATCTCCACACGGCAACT 672
Db	1319 GTCAAGATGACCCCTTCCTGCTCGCAGCATATGCAATGTCTCTCACAGCCCGCAGCG 1378
Qy	673 CTTCCACCTCCACCAACCGCCTTTTCATGACAGCAGCGCGGCTCCGACTACTCGGACCT 732
Db	1379 CCGCCACCAACCGACGATGTAAATATGATGTGTGATCTGTCTAATTACTCTGATGCGC 1438
Qy	733 CGAGTTCTTCTCCACCGCTCTCCAGGCTTGTGTAGCTTCTTCCAAAACGACTTTTACA 792
Db	1439 GAGATCTTACCTCCACCATCCCTGCTGTCTTCTTGCTTCGAGAGCACATTCAC 1498
Qy	793 TACGAGAGCTAGCTAGAGCAACCAATGGTTTCTCCGAGCGCAACTTTAGACAAGGC 852
Db	1499 TACGAAAGACTGTGAGGCTACTGATGATTTCTCGATGTAAATCTCCTTGACAGAGT 1558
Qy	853 GGGTTCGTTACGTGACAAAGGTGTGTGCTTGTGAGGAAAGAAAGTTCTGTGAGGAG 912
Db	1559 GGTTTGGCTATGTTTACAGAGGATGTCTTAAATGGCAAAAGAGATGCTGTAAACGA 1618
Qy	913 TTGAAAGTTGGAGTGTGCAGGAGAGAGGAGATTTTACGCAAGGTTGAATCATCAGC 972
Db	1619 TTGAAACTGGGAAGTGGCCAGGAGAGCGTAGAGTTTCCAGGCTGAGGTTGAATTAACG 1678
Qy	973 AAGGTTACACACAGGCACTGTGTGTCTCTTGTGGTATTGTCATCGCCGCTGCCAAAGA 1032
Db	1679 CGAGTACATACAAACCTGTGTCTTTGTGTGCTATTTGCAATTTCTGGAAGCAAGAG 1738
Qy	1033 TTGCTGTCTATGAGTTTGTCTTCAACACCAATCTCGAGCTTCACTTCATGCGAGGGA 1092
Db	1739 CTGCTGTCTATGAGTTTGTCTTCCCAATTAACCATTTGCAATTCATGCGAAAGGT 1798
Qy	1093 CGGCGCTTACAAATGAAATGGAAGCACCAATTTGAAGTTGCTCTTGATCTGTAAAGACTT 1152
Db	1799 CGACCAACAATGAGGTGGCCCTGTAGATTAAGATCAAGTTGGGCTGCGCAAGGTTTA 1858
Qy	1153 TCTTATCTTCAATGAAGTTGCAATCTTAAATTCATTCACGATATCAAGGCTTCAAC 1212
Db	1859 GCTTATCTTCAATGAAGCTGCAATCCAAAGATCATCTGTGACATTAAGGCAATCTAAC 1918
Qy	1213 ATATTGATAGATTCAAGTTTGAAGCTTAAGTTGCTGATTTTGTCTTGTCTAAGATTGCT 1272
Db	1919 ATTCTTCTTGACTTCCATTTGAAGCTTAAGTTGCTGACTTTTGGACTTGCACAAAGTTCACT 1978
Qy	1273 TCTGATACAAACACGATGTATCAACAGTGTGATGAGAACTTTGGGTAATTTGGGCTCG 1332
Db	1979 ACTGATTAACAACACCATGTTTTCGACAAAGTAATGGGCACTTTGGGATATTTGGCACT 2038
Qy	1333 GAATACGTTGAACGGGAAAGCTACGGAAGAGTGTGACGTTTCTCATTTGGCGTTGAG 1392
Db	2039 GAGTATGATCTTTCTGGCAAGCTAACGAAAAATCCGATGTATTTTCTTCCGAGTCATG 2098

Oy	1393	CTTTGGAGCTCAATTACTGACGTCGACCCTGTGATGCCAACAATGTCATGTAGATGAC	1452
Db	2099	CTTCTTGAGCTTAATTACTGGCGGGGCACAGTTGACACAACCCAAACATATATGATGAC	2158
Oy	1453	AGCTTAGTTGACTCAGGGAACGACCATTTGGTTAACGAGCATCTGACAGAGAATTGAG	1512
Db	2159	AGCTTGTTGACTGGGCAAGGCCATTACTGATGCGAGACCTTGAGGATGTTAATAATGAT	2218
Oy	1513	GTTTTAGCTGATGCAAAAGATGAATTAATGGATATGACAGAGAGAGATGGCTGCAATGTT	1572
Db	2219	GCTTATGTGATCTCGGCTGGAAAGSACTTCATCCTTAATGATATGGCAAGATGATA	2278
Oy	1573	GCATTGCTCGGCTTGTGTTGCTCCATTCACTGCGCGCACACTTCGCATGAGCCAGATT	1632
Db	2279	GCCCTGTCGACTGATGTGTACCGCATTTCTCAGCTCGTCGGCCACGATAGTCAGGTC	2338
Oy	1633	GTCGCTGCTGTTAGAGAGAAATGTATCACTGTCAGATCTTAAGAAAGGATGAGACCAGT	1692
Db	2339	GTTCCGGGCTTTGGAGGGCCAATGTCTTTGGAGAGCCTTAATGAAGGTTGCGGCTGGC	2398
Oy	1693	CAAAACAATGTATACAGCTCATACGAGAGAACCCGATTATGACTCGAGCCAGTACAAT	1752
Db	2399	CATAGCCGCTTCTTTGGGTATAC--AGACGCTCCGATTACGATTTCTGGCCAGTACAC	2455
Oy	1753	GAAAGATGAAAGAGTTTAGAAAAATGGCACTTGAACTGAAGATCAACGCCACGGGT	1812
Db	2456	GAGGACATGAAGAAAGTTCAAAGAAATGGCAATT-----CAACAACAATTATACGACAGC	2509
Oy	1813	GAGTACAGTAAATCCGACCACTGACTATGACCTGATACCCGTTGGTTCAAGACGAGGAC	1872
Db	2510	CAATTACGCGCCCAACCACTGAAATATGACAGATACCTGTCATCAAGCAGCGAGGAC	2569
Oy	1873	CAAAACACACGCGAAATGGAGATGGGGAATTAAGAGAAACCGTCAAGGCTTATAG	1928
Db	2570	CACACAGACCGAGAGATGGAGTGGGTGCAATGAAGAAAGTGGCTACAGTGTGG	2625

RESULT 10
US-10-437-963-6708/c
Sequence 6708, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 2003-05-14
SEQ ID NO 6708
LENGTH: 2187
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_13372C.1
US-10-437-963-6708

Query Match	Best Local Similarity	Score	DB	Length
Matches 847; Conservative	66.7%; Freq. No. 6.9e-150;	566.6;	17;	2187;
			Indels	Gaps
			404;	18;
				2;
QY	523	CCCTCCGACACTCTCTCTGTGTCCTCCAAAGCCGAGAGACCTTACGGTGGACAGACAGACAA	582	
Db	1595	CCGCGCGCGCGCGCGCGCGCGCGCTTCAAAAGGGGATCACTATGTTGGGGTGTACCAAAAT	1536	

QY	583	TGGCGGCAACAAAGCAACACCGCTGAGTCAATGTGTGTACGTCACTACCAACACCA	642
Db	1535	TGGCAGAAAATAGTCTCTCACTCCACTGATCATGTGTAAAGAGGTGCTTCGCAT	1476
QY	643	CCTAAGGCTTCATCTCCACCAACGGCAACCTGCTCCACTCCACCAACCGCTTTCATGAGC	702
Db	1475	CCCTCCCTCC-----ACCACCTCCGTGCTCACTAAATGTACACAGTGT	1433
QY	703	AGCAGCGGCGGTCCGACTACCTCGAACCGGTCCAGTCTTCTCCACCGTCCAGGCTT	762
Db	1430	GGTTCGTGCTCAAAATTACTCCGGTGGCAACACGCCAACCCTGATGTGCACCTGTGTCT	1371
QY	763	GTTTAGGCTTCCAAAAGCATTTCCATATCAGAGAGCTAGTAGAGCCACCAATGAT	822
Db	1370	GGATTGGTTTTTCAAGGTGATCTTCACTTAATGAGGACTTTCACGGCGACCAATGGA	1311
QY	823	TTTCCGAGCGCACTTTTAGACAAAGCGGGTTCGTTACGTGCACAAAGTGTGTTG	882
Db	1310	TTCTCCGATGCTAACTGCTCGGACAGGGCGGTTTTGGGTAAAGTTTCAAAAGAGTTCTG	1251
QY	883	CCTAGTGGAAAAGATGCTGTGAAGCAGTTGAAGTTGGAGTGGTACGAGGAGAGG	942
Db	1250	CCGAAATGGGACAGAGTGTCTGTGAAGCAATTTGAAGATGGAGTGGGACAGGAAGGT	1191
QY	943	GAGTTTCAAGCAGAGGTTGAGATCATCAGCAGAGTTCCACACGAGCATCTGTGTCTT	1002
Db	1190	GAAATTCAGGCGGAGGTGAGATTATCCAGCGGGTATCATCAACACATCTGTAACTTG	1131
QY	1003	GTTGGTTTATGATGCGCGGTGCCAAAAGATTGCTGTCTATGATTTGTTCTTAACAC	1062
Db	1130	GTTGGTTATTCATTTCTTGAGAGGAGAGGTTCCTGTCTATAGATATGTTTCCAAACAC	1071
QY	1063	AATTCGAGCTTCACTTCATGCGAGGAGCGGCTACAAATGAATGAGACACAGATTG	1122
Db	1070	ACATTGAGCTCCACTTCATGAGGAGAGCGGACCAACCATGGAATGGCTTCAACAGTTA	1011
QY	1123	AAGATGTGCTTGGATCTGCTTAAAGACTTCTTATCTTCAATGAATTTGCAATCTTAA	1182
Db	1010	CGCATGCTTTGGGTGCTGCGAAGGAGTTGGCAATCTTCAATGAAGTTGGCATCTTAAG	951
QY	1183	ATCATTTACCGGTATATCAAGGCTTCAACATTTTGAATGATTTCAAGTTTGAAGCTAAG	1242
Db	950	ATCATTTACCGGTATATCAAGGCTTCAACATTTTGAATGATTTCAAGTTTGAAGCTAAG	891
QY	1243	GTTGTGATTTTGGTCTTGTCTTAAGATGCTTCTATACAACACGATGTATCAACAGT	1302
Db	890	GTTGTGATTTTGGTCTTGTCTTAAGATGCTTCTATACAACACGATGTATCAACAGT	831
QY	1303	GTTATGGGAACCTTTGGGATCTTGGGTCCTGGAAATAGCTGCAACGGAAAGCTACGGAG	1362
Db	830	GTTATGGGACATTTGGGTACTTGGACACAGATGTGTGCTTCTGCGACGCTAAGCTGAG	771
QY	1363	AAGTTCAGTTTTCTCAATTTGGGTTGTGTTTGGAGCTCATTTACGACGTGACCC	1422
Db	770	AAATTCAGTTTTCTTCTTCTGCGAGTATGCTTCTTGAAGTAACTGGCCGCGCTCT	711
QY	1423	GTTATGCGAACATGCTATATGTATGATGACAGCTTAATGATCTGAGGACACATTTGCTT	1482
Db	710	GTTGATGCGAACATGCTATATGTATGATGACAGCTTAATGATCTGAGGACACATTTGCTT	651
QY	1483	AACGAGCATCTGAGCAGAGACTTTGAGGGTTTACTATGCAAGATGAATTAATGGG	1542
Db	650	ATGAGAGCATGATGATGAGCAATTAATGATCTTATGATTCACGGCTTAGAGACAGAG	591
QY	1543	TATACAGAGAGAGATGCTCGCATGTTGCTTGTGCTGCGGCTGTGTTCGCCATTCA	1602
Db	590	TACATAGTAAACAGATGAGGAGAGATGATCTTGTGCACTCTGTGTGAACGCCATTCT	531
QY	1603	GCTGCGCGAGACCTGCGATGAGCGCAATGTGTGCGGCTTAAAGAAATGATTAAGT	1662
Db	530	GCAAGCGGACGCCACGATGAGCGAGGTGTTCGGGCTCTTGAAGACGATGTGTCAATG	471
QY	1663	TCAATCTTAAAGAGGATGAGACCGAGGTCAAGAGCAATTTATACGCTATACGAGGA	1722

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|||||
Db 470 GATGATCGAAGAGAGTTCCTGCGCCATAGCCGATTCCTGGATTCATAC---AAC 414
|||
Qy 1723 AGCACCAGATTGACTCCAGCCAGTACATGAAGATGAGAAATGGA 1782
|||
Db 413 AGCAACGAGTACAGACGCGGCCATTACATGAAGACCTGAAGAAATTCAGGAAGTGGCA 354
|||
Qy 1783 CTTGGAACT 1791
|||
Db 353 TTTGGCACT 345
|||

RESULT 11
US-10-425-115-143391
; Sequence 143391, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 369326
; SEQ ID NO 143391
; LENGTH: 1316
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_6224C.1
; US-10-425-115-143391

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Query Match      27.0%; Score 524.8; DB 18; Length 1316;
Best Local Similarity 69.4%; Pred. No. 4e-138;
Matches 744; Conservative 0; Mismatches 322; Indels 6; Gaps 2;

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Qy 845 GACAGCGGGTGGTTAGCTGTCACAAAGTGTGTGGCTTGGAGGAAAGTTCGTG 904
Db 3 GCCACGCGTCCGCGAGCGCTGGGACAGAGATTGCTGCTTAATGGCAAGATTTGCTG 62
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Qy 905 TGAAGCAGTTGAAGTTGGAGTGGTTCAGGAGAGAGAGAGATTTCAGGACAGGTTGAGA 964
Db 63 TAAACCAATTAACTTGAAGCGGCCCAAGAGACCGGATTCAGGCTAGGTTGAGA 122
|||
Qy 965 TCATCAGCAGATTCCACCACAGGATCTGTGTCTCTTGTGGTTATTCATTCGCGGTG 1024
Db 123 TTATCAGCGGATCATCACAACATCTTGTGTCTTGTGGTTATTCATTCGCGGTG 182
|||
Qy 1025 CCAAAAAGTTGCTGTCTATGATGTTTCTTAAACAACATCTGAGCTTCACCCGCTAG 1084
Db 183 GCAAGAGGTGCTGTCTATGATGTTTCTTAAACAACATCTGAGCTTCACCCGCTAG 242
|||
Qy 1085 GCGAGGAGCGGCTTCAATGAATGAGTACAGACAGATTAAGATCTCTTGGATTCGTA 1144
Db 243 GGAAGGATGACCAATGAGTGGCCCACTAGTTAAAGTTCCTGCGGTGCGCA 302
|||
Qy 1145 AAGACCTTCTTATCTCATGAAGATTGCAATCTTAAATCAATTCACCGTATTCAGG 1204
Db 303 AGGGTTAGCTTATCTTATGAAGCTGCGCATCCAAGATTCATCCACCGCATTTAAG 362
|||
Qy 1205 CTTCAACATATGATGATTTCAAGTTTGAAGCTTAAGTTGCTGATTTGGCTTGGTGA 1264
Db 363 CATCTAACATCTTCTTGAATTCATTAATTTGAAGCTATGTTGCTGATCTTGGATGCA 422
|||
Qy 1265 AATTTGCTTGTATCAAAACAGCATGTATCAACAGCTGTGATGGAACTTTGGGTACT 1324
Db 423 AGTTCACTACTGTATCAACACCATGTGTCAACAGAGTAAATGGGCACTTTGGGTATT 482
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Qy 1325 TGGCTTCGGAATACGCTGCAAGCGGAAGCTCAGGAAGTGTGACGTTTCTCATTTG 1384
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Db 483 TGGACCTGAGTATGACAGCATCTGGCAAGCTCACAGAAAAATCCGATGATTTCTTGG 542
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Qy 1385 GCGTTGTCTTTTGGAGCTCATTTACTGACGCTGACCCGTTGATGCCAACAATGTCTATG 1444
|||
Db 543 GAGTCATCTCTTGAAGCTTATTAATCTGGCGCGCAATTAAGACCAACCAATATTA 602
|||
Qy 1445 TAGATGACAGCTTATTTAGCTGGGACAGACCATTTGCTTAACCGACATCTGACCAAGAG 1504
Db 603 TGGATGACAGCTTGTGTTACTGTGGGCAAGGCCATTTACTGATGAGAGCGCTCGAGGATGTG 662
|||
Qy 1505 ACTTTGAGGTTTACCTGATGCAAAAGATGAATATGCGTATGACAGAGAGATGGCTTC 1564
Db 663 AATATGATCTTTTGGGATCTCTCGCTCGAAAGAACTTCATCTTATGAGATGGCAA 722
|||
Qy 1565 GCATGTTGCTTGTCTGTGGGCTTGTGTTCGGCATTCAGCTGCGGCAACCTCGCATGA 1624
Db 723 GAATGATACCTGTGGGCTGTGGTGTGATGCGCATTCGCAAGTCTCGGCCACGATGA 782
|||
Qy 1625 GGCAGATTGTGGGTGCTGTAGAAAGAAATGTAATCACTGTCAATCTTAAAGAGATGA 1684
Db 783 GTGAGTGTCTGGGCTTGTGAAAGGAGAGCTGTCTTGGAGAGACCTTAATGAAGTGTTC 842
|||
Qy 1685 GACCAAGTCAAAAGCAATGTATACGCTCATACGAGAAACACCATTTATGACTCGAGCC 1744
Db 843 GACCTGGCCATAGCCGCTCTTTGGGTCAATA--TAGACGCTCTGATTAAGATTCGCGGC 899
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Qy 1745 AGTACATGAGACATGAAAGAAATTTAGAAAATGCGACTTGGAACTCAAGATCAACG 1804
Db 900 AGTACACAGGACATGACAGAAATTCAGAAAGCGCGCTT--CAATACACACCTTACA 956
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Qy 1805 CCAAGGTTGATGATGATTCGACAGTACTATGATGATGATCCCTGTGTTCAAGCA 1864
Db 957 CCGACAGCCATATCAGCGGCCCAACAGTAAATAGGCCAGAGTCCGTCTGATCAAGCA 1016
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Qy 1865 GCGAGGCGCAAAACACACACGCGAAATGAGATGGGAAAGATTAAAGAACCGG 1916
Db 1017 GCGAGGCGCCCGACAGACGACAGATGAGTGTGGGTGACGATGAAGAAAGTGG 1068
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RESULT 12
US-10-424-599-71008
; Sequence 71008, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 71008
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35132C.1
; US-10-424-599-71008

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Query Match      26.6%; Score 516.8; DB 16; Length 1585;
Best Local Similarity 67.8%; Pred. No. 8.3e-136;
Matches 770; Conservative 0; Mismatches 357; Indels 9; Gaps 3;

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[illegible]

Query	Match	Score	DB	Length
Query Match	26.6%	516.2	DB 13	1902
Best Local Similarity	67.1%	1.4e-135		
Matches	747	Conservative	0	Mismatches 365; Indels 3; Gaps 1
Publication No. US20020199218A1				
GENERAL INFORMATION:				
APPLICANT: GORING, Daphne R. et al.				
TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES				
FILE REFERENCE: P 25,762-A USA				
CURRENT APPLICATION NUMBER: US/10/086,464				
CURRENT FILING DATE: 2002-02-28				
PRIOR APPLICATION NUMBER: US 10/069,304				
PRIOR FILING DATE: 2002-02-19				
PRIOR APPLICATION NUMBER: PCT/CA00/00966				
PRIOR FILING DATE: 2000-08-18				
PRIOR APPLICATION NUMBER: US 60/149,466				
PRIOR FILING DATE: 1999-08-19				
PRIOR APPLICATION NUMBER: US 60/159,122				
PRIOR FILING DATE: 1999-10-13				
NUMBER OF SEQ ID NOS: 27				
SOFTWARE: Patentln Ver. 2.1				
SEQ. ID NO. 10				
LENGTH: 1902				
TYPE: DNA				
ORGANISM: Arabidopsis thaliana				
FEATURE:				
NAME/KEY: CDS				
LOCATION: (1) .. (1902)				
US-10-086-464-10				
QY	730	CGTCCAGTCTTCCTCCACCCGCTTCGAGGGCTTGTTGATTAGCTTCCAAAAGCACTTTC	789	
DB	757	CGCCCAATTACCTCCCTCTTCCGCTCTCTAGCCCTCCGATTCAACAGACACTTTT	816	
QY	730	ACATACGAGAGCTAGCTAGAGCCACCAATGTTCTTCGAGGGGAACTTGTGTGGACAA	849	
DB	817	ACTTACCAAGAGCTCGCGGCTGCACACAGAGGTTTACGATGCTAACCTTTTGGACAG	876	
QY	850	GGCGGGTTCGGTTACGTGCACAAAGTGTGTTCCTAGTGGAAAAGATTGCTGTGAAG	909	
DB	877	GGAGGATTTGGGTATGTCATTAAGAGAGTCTTGCCTAGCGGAAAGAAAGTAGCAGTTAAG	936	
QY	910	CAGTTGAAAGTGGGAGTGTGCAGGGAGAGGGAGTTTCAAGGAGAGTTGAATCATC	969	
DB	937	AGTTTAAAGCGGTTAGCGGACCAAGAGAGGAGGATTTCAAGCTGAGGTGATATATT	996	
QY	970	AGCAGAGTTCAACACAGGACATCTGTGTCTTGTGGTTATTGTCATGCGCGTACCAA	1029	
DB	997	AGCGGTGACATCATCGGTATCTTGTTCCTTGTGTGATTTGATGATAGCTGATGACAG	1056	
QY	1030	AGATTGCTTGCTATGAGTTGTGTTCTTAAACAATCTTGAGCTTCACTTCATGCGGAG	1089	
DB	1057	AGGATTTGGTTATGAGTTGTGTTCTTAAACAACTTGGAAATATCATCTTCACTGAGAA	1116	
QY	1090	GAGCGGCTTCAATGGAATGAGAGCAGAGATTGAAGTTGCTGTGATCTGCTTAAAG	1149	
DB	1117	AATCTTCGGTAAAGAGGTTCTCCACATGTTGCGTATGCGCTTAAAGTGTGCGAAAG	1176	
QY	1150	CTTTCTTATCTTCAATGAAGATTGCATCTCTTAAATCATTCACCGTGTATCAAGGCTTCA	1209	
DB	1177	CTGCTTACCTTCAACGAAAGCTGCATCTCTCGGATCATTCACCGCGACATCAAGTCTGCA	1236	
QY	1210	AACATATGATGATGATTTCAAGTTTGAAGCTTAAAGTTGAGTTTGGTCTTGTCTAAGATT	1269	
DB	1237	AATATTTCTTGTGACATTTCACTTGTATGCTATGAGTGTGATTTTGGATTAGCTTAAAGTTA	1296	
QY	1270	GCTTCTGATACAAACACGATGATCAACAACGTTGATGGAACCTTTGGGTACTTGAGCT	1329	
DB	1297	ACATCTGATTAACAACACTCATGATATCTACTCGTGTATGGAACTTTGGATATCTAAGCT	1356	
QY	1330	CGGAATAGCGCTCAGCGGAAGCTTACGAGAGAAAGTCTGACGTTTCTTCATTTGGCGTT	1389	
DB	1357	CCAGATATGCTTCAAGCGGTAAATTTAACCGAATAATTCGATTTTCTTCAACGAGATT	1416	

QY 1390 GTGCTTTGAGCTGATTAAGAGAGTGGAGCCGTTGATGCCAATGTCTATGTAGAT 1449
DB 1417 AGTTATTGGAACCTTAATACTGAAAAAGACCGGTTGAT--AAATGATACCATGAGC 1473
QY 1450 GACAGCTTAGTACTGGGACGACCATTTCTTAAACGAGCATCTGAGCAAGAGACTTT 1509
DB 1474 GACACCTTAGTATGATTTGGGCTCGGCTCTTATGGCTCGGCGCTAGAGATGAAACTTT 1533
QY 1510 GAGGCTTAGTCTGATGCAAAATGAAATAAGGATATGACAGAGAGAGATGGCTGAGATG 1569
DB 1534 AATGAGCTGACAGATGCGAGGCTTGAAGGCACTACACCCGCAAGAAATGCTGAAATG 1593
QY 1570 GTTGCTTTGCTGGGCTTGTGTGGCCATTCAGCTCGCCGAGACCTCGCATGAGCCAG 1629
DB 1594 GTGACTTTGGCCGCTGCTAGCATTCCTATGCGGCGTAAAGCTCAAAAGATGAGCCAG 1653
QY 1630 ATTGTCGCTGCTTAGAAGAAATGATCATCTGATCTTAAACGAGGAGTGAACCA 1689
DB 1654 AATGTAAGAGCTTAAAGAGAAAGTGTCTTATGATGCTTAAACGAGGCTGAAGCCA 1713
QY 1690 GGTCAAGAGATGTATACAGCTCATACGAGAGACCGATTTATGATCTGAGCCAGTAC 1749
DB 1714 GGACACAGTAACGTTTACGGGCTATGGGAGCAAGCTCGGATTAATGTCAGACATCTTAC 1773
QY 1750 AATGAAGACATGAAAGATTAGAAATGCACTTGAACCTCAAGATACAAAGCCACG 1809
DB 1774 AATGCAAGACATGAAGAAATTCAGACAGATAGCTTTGTCGAGCCAGAAATTCACAGTCACT 1833
QY 1810 GGTGAGTACAGTAATCCGACAGTGAATGGA 1842
DB 1834 GACTGTGAAGAAACATCTAGTAATGATTCTAGA 1866

RESULT 14
US-10-086-464-9
; Sequence 9, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1939
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-086-464-9

Query Match 26.6%; Score 516.2; DB 13; Length 1939;
Best Local Similarity 67.1%; Pred. No. 1.4e-135;
Matches 747; Conservative 0; Mismatches 363; Indels 3; Gaps 1;
QY 730 CGTCCAGTTCTCTCTCCACCGTCTCCAGGCTTGTGTGGCTTCTCCAAAAGCACTTTC 789
DB 774 CGGCCAGTTTACCTCTCTCTCTGCTGCTAGCCCTCGAATCAACAAGACACTTTC 833
QY 790 ACATACGAGAGAGTACTAGAGCCACCAATGTTTCTCCAGGCGCAACTGTATGAGACA 849
DB 834 ACTTACCAAGAGGCTTGGCGCTGCAACAAGAGGGTTTACGATGCTAACCTTTGGGACAG 893
QY 850 GCGGCGTTGGTTACGTGCAAAAGGTGTGTGCTTATGGGAAAGAAAGTTGCTGTGAAG 909

DB 894 GGAAGATTTGGGTATGTCATTAAGAGAGTCTTGCTTACGGGAAAGAGATGACATTAAG 953
QY 910 CAGTTGAAAGTTGGAGAGTGTCCAGGAGAGAGGAGTTTCAGGCGAGAGTTGAGATCATC 969
DB 954 AGTTTAAAGCGGGTACGGGCAAGAGAGAGGGGTTTCAAGCTGAGGTCATATCATTT 1013
QY 970 AGCAGAGTTCCACACAGGCACTTGGTGTCTCTGTGTGTTATGTGATCGCCGGTCCAAA 1029
DB 1014 AGCCGTGTGCATCATCGGATTCCTTGTCTTTGTTGGATATTTGCATAGCTGATGAGCAG 1073
QY 1030 AATGTCCTGTCTATGAGTTTGTCTTAAACAACAAATCTGAGCTTCACTCCATGAGCGAG 1089
DB 1074 AGCATGTTGTTTATGAGTTTGTCTTAAACAAACCTTGGAAATCATCTTATGAGGAAA 1133
QY 1090 GGACGCGCTTACAAATGAAATGAGACACAGATTGAAGATTGCTTTGATCTGCTAAAGGA 1149
DB 1134 AATCTTCCGGTATGAGATTCTCCACTAGTTGCGTATGCGCTTATGAGTCTGGAAGGA 1193
QY 1150 CTCTTATCTTATGAGAAATGCAATCTCTAAATGATTCACCGGTATTCAGAGCTTCA 1209
DB 1194 CTGCTTACCTTACAGAAACCTGCAATCTCGGATCATTCACCGCATCAAGTCTTGA 1253
QY 1210 AACATATGATGATTTCAAGTTTGAAGCTTAAGTTGCTGATTTTGTCTGTAAGATT 1269
DB 1254 AATATCTCTTGAACCTTCAACTTTGATGCTATGCTGCTGATTTGGATTAAGCTTAAGTTA 1313
QY 1270 GCTTCTGATACAAACAGCATGTATCAACAGCTGTATGAGGAACTTTGGGTACTTGGCT 1329
DB 1314 ACATCTGATTAACAACCTCATGTATCTACCTGCTGATGAGGAACTTTGGATTTATGCT 1373
QY 1330 CCGGAATAGCGCTGCAAGCGGAAAGCTCAGGAGAAAGCTGACGTTTCTCATTTGGGCTT 1389
DB 1374 CCAAGATATGCTTCAAGCGGTAATTTATTAACCGAAGAAATCCGATGTTTCTTACGGAGTT 1433
QY 1390 GTGCTTTGAGCTCATTAAGCTGACCGCTGATGCCGTTGATCCAAATGCTATGTAGAT 1449
DB 1434 ATGTTATTGGAACCTTAATACTGAAAAAGACCGGTTGAT--AATACATCACCATGAGC 1490
QY 1450 GACAGCTTAGTGACTGGGACGACCACTTGTCTTAAACGAGATCTGAGCAAGAGACTTT 1509
DB 1491 GACACCTTAGTGAAGTTGGGCTCGGCTCTTATGAGCTGCGGCTGTAAGAGATGAAACTTT 1550
QY 1510 GAGGCTTACGTATGCAAAAGATGAATATGATGATGACAGAGAGAGATGCTCGCATG 1569
DB 1551 AATAGCTCGAGATGAGAGGCTTGAAGGCACTTAACCCGCAAGAAATGCTCGAATG 1610
QY 1570 GTTGCTTGTGCTGCGGCTTGTGTGCTCCATTCAGCTGCGCAACTCGCATGAGCCAG 1629
DB 1611 GTGACTTGTGCGCTGCTGCTAGCATTCGTCATTTCGGGCGTAAACGTCCAAAGATGAGCCAG 1670
QY 1630 ATTGTCGCTGCTTGAAGAAATGTATCACTGTCAATCTTAACGAGGAGATGAGACA 1689
DB 1671 ATAGTAAGAGGTTTGAAGAGAGAGATGTCTTGAATGCTTAAAGAAAGGTGTGAAGCA 1730
QY 1690 GGTCAAGCAATGTATACAGCTCATACGAGAGAGACCGAATATGACTGAGCCAGTAC 1749
DB 1731 GGACACAGTAAAGTTTACGGGCTATTTGGAGAGAGCTCGGATTAATGACAGCATCTTAC 1790
QY 1750 AATGAAGACATGAAGAGTTTGAAGAAATGCGCACTTGAATCTCAAGAGTACAAGCCACG 1809
DB 1791 AATGCAAGACATGAAGAAATTCAGACAGATAGCTTTGTGAGCCAAAGAAATTCACAGTCACT 1850
QY 1810 GGTGAGTACAGTAATCCGACAGTGAATGGA 1842
DB 1851 GACTGTGAAGAAACATCTAGTAATGATTCTAGA 1883

RESULT 15
US-10-739-930-726
; Sequence 726, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
 ; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53377)B
 ; CURRENT APPLICATION NUMBER: US/10/739,930
 ; CURRENT FILING DATE: 2003-12-18
 ; NUMBER OF SEQ ID NOS: 11088
 ; SEQ ID NO 726
 ; LENGTH: 2185
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: ARATH-23APR03-CLUSTER71836_1
 US-10-739-930-726

Query Match 26.68; Score 516.2; DB 18; Length 2185;
 Best Local Similarity 67.1%; Pred. No. 1.5e-135;
 Matches 747; Conservative 0; Mismatches 363; Indels 3; Gaps 1;

QY 730 CGTCCAGTTCTCTCCACCGCTCTCCAGGGCTTGTAGGCTTCTCCAAAGCACTTTC 789
 Db 871 CGCCCACTTTTACCTCTCTCTGCGCTCTAGCCCTCCGATTCACAGAGCACTTTT 930
 QY 790 ACATACGAGAGCTAGCTAGAGCCACCATGTTTCCGAGGCGAATTGTTAGACAA 849
 Db 931 ACTTACCAAGAGCTTGGCGCTGCAACAGAGGCTTTACGATCTAACCTTTTGGAG 990
 QY 850 GGGGGTTCGTTACGTGCAAAAGTGTGTTCTAGTGGAAAGAGTTGCTGTGAAG 909
 Db 991 GAGGAGTTTGGGTATGCTTAAGAGTCTTCTAGCGGAAAGAGTAGCACTTAAG 1050
 QY 910 CAGTTAAAGTTGGAGTGTGTCAGGAGAGAGGAGTTTCAGGCAAGGTTGATCATC 969
 Db 1051 AGTTTAAAGCGGTTAGCGGACAGAGAGAGGAGTTTCAGCTGAGTGCATATCAT 1110
 QY 970 AGCAGAGTTTACACAGGCACTGTGTCTCTGTTGTTATGATCGCCGCTGCATA 1029
 Db 1111 AGCCGTGTCATCATGATGATCTGTTTCTTGTGTTGATGATGATGATGATGATG 1170
 QY 1090 AGATTGCTGTCTATGAGTTTGTCTTAAACAATCTGAGCTTCACTCCATGCGAG 1089
 Db 1171 AGGATGTTGGTTATGAGTTTGTCTTAAACAATCTGAGATCATCTTCAATGGAAA 1230
 QY 1090 GGACGGCTTACAAATGGAATGAGCAACCAATTTGAAGATTCTTGGATCTGCTAA 1149
 Db 1231 AATCTTCCGTTATGAGATTCTTCACTAGTTCGATTCGCTTGGTCTGCAAGGA 1290
 QY 1150 CTTTCTTATCTTCAAGATGATGCAATCTTAATCATTCACCGTATATGAAGCTTCA 1209
 Db 1291 CTGCTTACCTTCAAGAGATGCTCCATCTCGATCATTCACCGGACATCAAGTCTGCA 1350
 QY 1210 AACATATTGATGATTTCAAGTTGAAGCTAAGTTGCTGATTTTGTCTTGGCTAAGAT 1269
 Db 1351 AATATTTCTTGGACTTCAACTTATGATGATGATGATGATGATTTTGGATTAGCTA 1410
 QY 1270 GCTTCTGATACAAACAGCATGATATCAACAGTGTGATGAGGAACTTTGGGTA 1329
 Db 1411 ACATCTGATTAACAGACTCATGATCTACTGCTGATGAGGAACTTTGATATCTAGCT 1470
 QY 1330 CCGAATATGCTGACAGCGAAAGCTCAAGGAAAGTCTGAAGTTTCTCATTTGGGCTT 1389
 Db 1471 CCAGAAATATGCTTCAAGCGGTAATTAACGAGAAATCCGATTTTCTTTACGAGTT 1530
 QY 1390 GTGCTTTTGGAGCTCATTTACTGAGAGTGAACCGCTGATGCAACATGCTATGAT 1449
 Db 1531 ATGTTATTTGAATTTAATCTGAGAAACGACCGTTGAT--AATAGCATACCATGAC 1587
 QY 1450 GACAGCTTAGTTGAGTGGGACGACCATGCTTAAACGAGATCTGAGCAAGGACCTT 1509
 Db 1588 GACACCTTAGTATGATGGCTCGGCTCTTATGCTGCGGCTAGAGAGATGAGAACTTT 1647
 QY 1510 GAGGGTTTACCTGATGCAAAAGATGATATGAGTATGACAGAGAGGATGGCTCGCAT 1569

Db 1648 AATGAGCTCGAGATGCGAGGCTTGAAGGCACTTAACCCGCAAGAAATGGCTCGATG 1707
 QY 1570 GTTCTGTGTGCTGGGCTTGTGTTTCCCATTCAGCTCGCCGACAGCTCGCATGAGCC 1629
 Db 1708 GTGACTTGTGCGCTGCTAGCATTCGTCATTTGGGGGCTTAACGTCGCAAAATGAGCC 1767
 QY 1630 ATTGTGGTGGCTTGAAGAAATGATCATGTCAGATCTTAAAGAAAGATGAGACCA 1689
 Db 1768 ATAGTAAAGAGCTTGAAGAGAGAGTGTCTTATGATGCTTAAAGAAAGTGTGAAGCCA 1827
 QY 1690 GGTCAAGCAATGATACAGCTCATACGAGAGAGACCCGATTAATGACTGAGCAGATAC 1749
 Db 1828 GGAACAGATACGTTTACGGGTATTTGGAGACAGCTCGATTAATGATCAGACATCTTAC 1887
 QY 1750 AATGAAACATGAAAGAAAGTTTGAAGAAATGAGCACTTGAAGCTCAAGAGTACAAAGCCAG 1809
 Db 1888 AATGCAACATGAAAGAAATTCAGACAGATATGCTTTGTGAGCCAAAGATTCGAGTAC 1947
 QY 1810 GGTGATACAGTAAATCCGACAGTGAATGAGA 1842
 Db 1948 GACTGTGAAGAAATCTAGTAAATGATTCTAGA 1980

Search completed: November 13, 2004, 12:36:53
 Job time : 699 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 07:54:05 ; Search time 4165 Seconds
(without alignments)
17008.125 Million cell updates/sec

Title: US-10-069-304-1

Perfect score: 1944
Sequence: 1 atgctctgcgcgcctctcc.....atagtgacctctctcttaa 1944

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1342.6	69.1	2106	3 CNS0A4OX	BX823746 Arabidops
2	594.6	30.6	723	6 CD839231	CD839231 RPO2.1141
3	572.8	29.5	853	5 BX834233	BX834233 BX834233
4	496	25.5	1036	5 BX837083	BX837083 BX837083
5	442.2	22.7	759	4 BM408099	BM408099 EST582426
6	438.2	22.5	799	7 CN010757	CN010757 WHE3875_G
7	429.6	22.1	757	4 BG596561	BG596561 EST495239
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12	409.4	21.1	788	7 CF436437	CF436437 EST672782
13	408.6	21.0	1084	5 BP184771	BP184771 BP184771
14	405.6	20.9	789	7 CF436655	CF436655 EST673000
15	403.8	20.8	827	7 CN816079	CN816079 HRO4516_F
16	400	20.6	666	4 BM358715	BM358715 GA_Ba001
17	399	20.5	573	1 AV551753	AV551753 AV551753
18	397.2	20.4	824	6 CD435142	CD435142 ELU1N0355
19	396	20.4	785	7 CF436122	CF436122 EST672467
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21	383.8	19.2	695	6 CA072174	CA072174 SCCAM100
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25	369.4	19.0	611	6 CA237156	CA237156 SCMCFL500
26	367	18.9	618	3 CA269355	CA269355 SCBGR307
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28	365	18.8	762	7 CO201810	CO201810 RTCNT2_8
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30	361.8	18.6	890	7 CO114544	CO114544 GR_Eb015
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32	356.2	18.3	652	5 BO849683	BO849683 OGB10120
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34	355	18.3	769	7 CK283399	CK283399 EST746121
35	350	18.0	693	6 CA164704	CA164704 SCBRL2312
36	349.8	18.0	671	6 CA237152	CA237152 SCMCFL500
37	348.2	18.0	593	2 CF015663	CF015663 EML_4_B10
38	348.6	17.9	595	5 BQ240617	BQ240617 TA050515B
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41	347.2	17.9	682	6 CA999610	CA999610 S345P_H09
42	346.8	17.8	622	6 BQ404121	BQ404121 GA_ED006
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ALIGNMENTS

RESULT 1
LOCUS CNS0A4OX
DEFINITION Arabidopsis thaliana full-length cDNA complete sequence from clone GSUTLS712E12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).

ACCESSION BX823746.1 GI:42462388
VERSION HTG; GSUT CDNA.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana

REFERENCE Castellani V., Aury J.M., Jallion O., Wincker P., Clepet C., Menard M., Craud C., Caboche M., Weissenbach J., Schachter V., Temple G., Caboche M., Weissenbach J. and Salanoubat M. (1999) The Arabidopsis genome: a complete sequence of the Arabidopsis thaliana genome. *Genome* 42: 1-10.

TITLE Whole Genome Sequence Comparisons and Full-length cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2106)

GENOSCOPE.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castellani V., Aury J.M., Jallion O., Wincker P., Menard M., Craud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information Center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES

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RESULT 2
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DEFINITION RFO2.114104.F010529 RFO2 Brassica napus cDNA clone RFO2114104, mRNA
SEQUENCE
ACCESSION CD839231
VERSION CD839231.1 GI:32521171
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 723)
Genoplatne.
Genoplatne, a major partnership french program in plant genomics
Unpublished (2003)
CONTACT: Genoplatne
Genoplatne
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>
and <http://genoplatne-info.intobio.gen.fr>).
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Best Local Similarity 99.3%; Pred. No. 1.4e-135;
Matches 597; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1764 GAAGTTAGAAATATGCACTTGGAACTCAAGAGTATACGCCCGGGTATGATCACTTAA 1823
DB 421 GAAGTTAGAAATATGCTTGGAACTCAAGAGTATACGCCCGGGTATGATCACTTAA 480
QY 1824 TCCGACCAATGATGACTGATCCCGTCTGTTCAAGCAGCAGGAGGCAACCAACAGC 1883
DB 481 TCCGACCAATGATGATGATCCCGTCTGTTCAAGCAGCAGGAGGCAACCAACAGC 540

QY 1894 CGAAATGAGATGGGGAAGATTAAAGAACCCGTCAGGTTTATAGTGAACCTTCTCTTAA 1943
DB 541 CGAAATGAGATGGGGAAGATTAAAGAACCCGTCAGGTTTATAGTGAACCTTCTCTTAA 600
QY 1944 A 1944
DB 601 A 601
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BX834233/c
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DEFINITION BX834233 Arabidopsis thaliana Adult vegetative tissue Col-0
ACCESSION BX834233
VERSION BX834233.1 GI:42517711
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 853)
Castelli,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Querier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished (2004)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction; Temple G
Genoscope members carried out sequencing and annotation; Castelli
V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences).
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
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Sequences),
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.
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Db	79	CCCTCTCCACAACACT	138
OY	151	TCTTTCGCTCTACACTTTCCT	210
Db	139	CCT	198
OY	211	TCTCCACT	270
Db	199	ACT	255
OY	211	GCACTGTATCT	330
Db	256	CCCAACCAACCTCTAAACCTCTGAAGCCCTCTCATCTCTAACCAAGACCAACCAACCT	315
OY	331	CCCTCAGCGAAGAGAGATCTCTCTGACCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCT	390
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OY	391	TCCGACGGTTTATCAACAGAGATGTGTGGGAATGCGCATTCGAGAGATCGCTCTGCT	450
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OY	451	GTGATAGTACTCTGATTTGTCTCTCTGTAAAGAAACGACGGAGA-----GACGAA	504
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OY	505	GAAAGATGCTTACTATGTTCTCTCGGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	564
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Qy 922 GGGAGGTGTGAGGAGAGAGAGTTTTCAGAGAGTTGATATCATGACAGAGTTTTC 981

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Qy 982 CA 983

Db 973 AA 974

RESULT 5
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DEFINITION BM408099 potato roots Solanum tuberosum cDNA clone cFR033021 5'
end. mRNA sequence.
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VERSION BM408099.1 GI:18259729
KEYWORDS EST.
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ORGANISM Solanum tuberosum
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asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 759)
van der Hoeven, R., Sun, H., Karameycheva, S.A., Tsai, J., Van Aken, S.,
Uiterback, T., Chiemung, A., Bougri, O., Buell, C.R., Rinning, C.,
Tankisley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatocenter@igir.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.
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SOURCE location/Qualifiers
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XhoI; supplier: Cornell University, Tankisley lab;
sequencing: The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after plucking the stem
cuttings from in vitro grown plants on medium."

ORIGIN
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Best Local Similarity 73.9%; Pred. No. 5.9e-98;
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Db 61 TGTGTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

Qy 1053 TCTTACACAAATCTTCGAGCTTCACTCCATGCGGAGGAGCGCTTACATGAATGAG 1112

Db 121 TCCAAACAATCTTGGATATTTTACACGGAAGAGAGGCTCTTTGGATTGCGC 180

Qy 1113 CACGAGTTGAAGATGCTTGTGATCTGTCTTAAGAGCTTTCTTCTTCAAGAAATG 1172

Db 181 AATACGCTAAGATGCTTGTGATGCTTGAAGAGCTTGAATCTGCAAGAAAGC 240

Qy 1173 CAATCTTAAATCATATTCACCGGATATCAAGGCTTCAACATATGATGATTTCAAGT 1232

Db 241 CCAACCGAAATCATATTCACCGGATATCAAGGCTTCAACATATGATGATTTCAAT 300

Qy 1233 TGAAGCTAAGTGTGCTGATTTTGTGCTTGAAGATGCTTGAATACAAACAGCAT 1292

Db 301 TGAGGCTAAGTGTGCTGATTTTGTGCTTGAAGATGCTTGAATACAAACAGCAT 360

Qy 1293 ATCAACAGGTGATGAGAACTTTGGTGTGCTTGGCTCCGAAATACGCTGCAAGCGAA 1352

Db 361 CTCACCAAGAGTGAAGAACTTTGGTGTGCTTGGCTCCGAAATACGCTTCCGAA 420

Qy 1353 GCTCAGGAGAACTGACGTTTCTCATTTGGCGTGTGCTTGGAGCTTATTCTG 1412

Db 421 GCTTACAGACAAAGTACAGCTTATCTCTTGTGTAATGCTTGTGATGATTAATCG 480

Qy 1413 ACGTGACCCGTTGATGCCAACATGCTATGATGATGACAGCTTATGATGATGATG 1472

Db 481 ACGTGACCCGTTGATGCCAACATGCTATGATGATGATGATGATGATGATGATG 540

Qy 1473 ACCATTGCTTAAACGAGATCTGACAGAGAGAGAGCTTGAAGGTTTGAAGTGAAGT 1532

Db 541 TCCATTACTCACAGAGCTTTGAAGATGAAGAAAGTTGATACCTTGTGATGCTGCGT 600

Qy 1533 GAATATGCTTATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1592

Db 601 AGAAATGATTTATAACCAATATGATGATGATGATGATGATGATGATGATGATG 660

Qy 1593 TCGCATTCAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1652

Db 661 GCGTATTCAG 720

Qy 1653 TGTATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1691

Db 721 TGTATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759

RESULT 6
CN010757 799 bp mRNA linear EST 29-MAR-2004
LOCUS CN010757
DEFINITION CN010757 wheat Triticum aestivum cDNA clone WHE3875_G12_M23, mRNA
sequence.
ACCESSION CN010757
VERSION CN010757.1 GI:45806789
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases 1 to 799)
Anderson, O.D., Zhao, S., Han, P.S., Heinen, S., Hsia, C.C., Kang, Y.,
Kruger, W.M., Izzo, G.R., Miller, S., Muehlbauer, G.J., Miller, R.,
Pritsch, C., Rausch, C.J., Seaton, C.L., Tong, J.C., Vance, C. and
Wilson, C.F.
The structure and function of the expressed spike cDNA library
Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: candersnpw.usda.gov
 Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20. No effort was taken to identify ESTs of fungal origin from this library, thus this EST could be of wheat or fungal origin.
 Seq primer: SK primer.
 Location/Qualifiers

FEATURES
 Source
 1..739
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Suma13"
 /db_xref="taxon:4565"
 /clone="WHE3875.G12.M23"
 /tissue_type="Spike"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /clone_lib="wheat Fusarium graminearum infected spike cDNA library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid pluscript SK; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Spikes were sprayed at anthesis with Fusarium graminearum. Total RNA, and poly(A) RNA were prepared and pooled from infected spike at 0, 6, 12, 24, 36 and 48 hours after inoculation, a cDNA library was made, and the cDNA clones were in vivo excised to give pluscript phagemids in G. Muehlbauer lab at the University of Minnesota (Kruger, W.M., Muehlbauer, G.J., Pritsch, C., Vance, C.). The cDNA library should contain genes of both wheat and fungal pathogen origin. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 22.5%; Score 438.2; DB 7; Length 799;
 Best Local Similarity 72.9%; Pred. No. 5.8e-97;
 Matches 577; Conservative 0; Mismatches 213; Indels 1; Gaps 1;

820 GATTTCCTCCGAGCGAAGCTTGTAGACAAAGCGGTTCCGTTACGTCACAAAGTGTG 879
 9 GGGTTCCTGATGCTAATCTCTCGGAC-AGTGGTTTGGATCTCTTCAAAAGAGTGTG 67
 880 TTGCTTATGGGAAAGAAAGTCTGTGAGAGAGTTGAAAGTTGGAGTGTGACGAGAG 939
 68 CTGCTTAATGCAAGAGATGCTGTGAAGCAATGAACTGGAGTGGCAGGAGAG 127
 940 AGGAGTTTCGAGAGGTTGAGATCATGCGAGAGTTCACAGGCAATCTGTGCT 999
 128 CGTAGTTCACGGGAGGTGAGATTAATCAGCGTGTCAACAGCAATCTGTGCT 187
 1000 CTTGTTGTTATTCATGCGCGGTGCCAAAGATTGCTTGTATGAGTTTGTCTTAC 1059
 188 CTGTTGGTTATCTGATCTCTGGGGGGAAGAGTTGCTTGTATGAGTTTGTACCAAT 247
 1060 AACCAATCTCGAGCTTCACTCCATGCGGAGGAGCGCTTAAATGGAATGAGACCA 1119
 248 AACCAATGGAATTCACCTTACATGGAAGAGCGGTCCAAAGTTGAGTGGCCATAGA 307
 1120 TTGAAGATTGCTTGAATGCTGCTAAAGAGCTTCTTATCTTCAATGAGATTGCAATCT 1179
 308 CTAAAGATTGCTTGGTCTGCTTGAAGGTTTGGCATTCATTCAGAAAGATTGCCACCG 367
 1180 AAAATCATTCACCGTATATCAAGGCTTCAAAATATATGATAGATTCAAGTTGAAGCT 1239
 368 AAGATCATACATCGATATTAAGTCATCAACATCTTCTTGAATTTAAATTCGAAGCT 427
 1240 AAGTTGCTGATTTTGTCTTGAATGCTTGTGATGATACAAAGCATGATATCAACA 1299
 428 AAGTTGCGGATTTTGTCTGCAAAAGTTCACTCTGATTAACAACACACATGTGCAACA 487
 1300 CGTGTGATGGACCTTTGGGACTTGGCTCCGGAATCGCTGCAAGGGGAAAGTCAAG 1359
 488 AGAGTAATGGCACTTTTGGTATTAAGACCAAGATATGCGCTTCTTGGAAAGCTAATCT 547

QY 1360 GAGAGTGTGACGTTTCTCATTTGGCGTGTGCTTTGGAGCTCATTAAGTCACTGCA 1419
 DB 548 GAGAAATCAGATGCTTTCTTTGGAGTGTGCTTTGAGCTGATTAAGTCACTGCACTG 607
 QY 1420 CCCGTTGATCCCAACATGCTTATGATGAGACAGCTTATTTGACTGGGACCAAGCT 1479
 DB 608 CCGTTGATTCACCCCAACATATATGATGACAGCTTGTGATTTGGGCAAGACTTTTA 667
 QY 1480 CTTAACCGAGCATCTGAGCAAGAGACTTTGAGGTTTACCTGATGCAAAAGATGATAT 1539
 DB 668 CTGATGAGACACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 727
 QY 1540 GGGTATGACAGAGAGAGATGCTCGCATGATGCTTGTGCTGCGGCTTGTGTCGCAT 1599
 DB 728 GATTTCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
 QY 1600 TCAGCTGCGCG 1610
 DB 788 TCAGCAGCTCG 798

RESULT 7
 LOCUS BGS96561 757 bp mRNA linear EST 07-MAR-2003
 DEFINITION EST495239 cSTS Solanum tuberosum cDNA clone cSTS15A23 5' sequence,
 mRNA sequence.
 ACCESSION BGS96561
 VERSION BGS96561.1 GI:13614701
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanales; Solanales; Solanum.
 1 (bases 1 to 757)
 van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chieningo, A.,
 Bougri, O., Buell, C.R., Romming, C., Tanksley, S. and Baker, B.
 Generations of ESTs from sprouting potato eyes
 Unpublished (2000)
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics
 Institute. Orders can be made through URL:
 http://genome.arizona.edu/orders/
 Seq primer: M13p-R.

FEATURES

Source
 1..757
 Location/Qualifiers

/organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cSTS15A23"
 /tissue_type="sprouting eyes from tubers"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="SOLR"
 /note="Vector: pluscript SK(-); Site 1: EcoRI; Site 2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."

ORIGIN

Query Match 22.1%; Score 429.6; DB 4; Length 757;
 Best Local Similarity 73.4%; Pred. No. 7.6e-95;
 Matches 549; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 901 GCTGTGAAGAGTGAAGATTGGGAGTGTGACGAGAGAGAGATTTCAGGACAGAGTT 960
 DB 1 GCGATTAAACAGCTTAAGCTGAGAGTGAAGTGAAGAGAGAGAGTGAATTCAGGCGGAGATT 60

QY 961 GAGATCATCAGCAGAGTTCCACACAGCATCTGGTGTCTCTGTTGGTATTGACATGCC 1020
Db 61 GAGATTATTATGCGAGATACATCACACATCTGTGTCTCTGTTGGTATTGACATCT 120
QY 1021 GGTGCCAAAGATTGCTGTCTATGAGTTTGTCTTACAAACAATCTCGATCTCACCTC 1080
Db 121 GGGGCTCAGAGCTGTGTGTATGAGTTTGTCTTACAAACAATCTTGGATTTCATTTA 180
QY 1081 CATGCGAGAGGAGCGGCTACATAGCAATGAGACACAGATTGAATGCTCTTGGATCT 1140
Db 181 CACGGAAGAGGAGCGCTCTCTTGGATTGCGCAATACGCTTAAGATTGCTTAGAGTCA 240
QY 1141 GCTAAAGACTTTTATCTTCAATGAGATTGCAATCTTAAATCAATTCACCGTATATC 1200
Db 241 GCTAAAGACTGCAATCTGATGATGAGACTGCAACCGAAATCAATTCACCGTATATC 300
QY 1201 AAGGCTTCAACATATTGATGATGATTCAAGTTTGAAGTGAAGTCTGATTTGGTCT 1260
Db 301 AAGGCTTCAACATATTGATGATGATTCAAGTTTGAAGTGAAGTCTGATTTGGTCT 360
QY 1261 GCTAAGATTGCTTGTGATACAAACAGCATGATTCACACGCTGATGAGAACTTTGGG 1320
Db 361 GCTAAGATTGCTTGTGATACAAACAGCATGATTCACACGCTGATGAGAACTTTGGG 420
QY 1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCAGGAGAGCTGATGCTTTTCTCA 1380
Db 421 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTTCAAGCAAGTCAATATCTCC 480
QY 1381 TTTGGCTGTGCTTTTGGAGCTCATTTACTGAGACGTCGACCCGTTGATGCCAACAATGTC 1440
Db 481 TTTGGCTGTGCTTTTGGAGCTCATTTACTGAGACGTCGACCCGTTGATGCCAACAATGTC 540
QY 1441 TATGATGATGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 541 TATGATGATGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 1501 GAGACCTTGAAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Db 601 GAAAGCTTGAATACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 1561 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 661 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 1621 ATGAGCGAGATTGCGCTGCTGAGAG 1648
Db 721 ATGAGCGAGATTGCGCTGCTGAGAG 748

RESULT 8
LOCUS CB655196
DEFINITION OSUNEC08f21.f OSUNEC Oryza sativa (japonica cultivar-group) cDNA
VERSION CB655196
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE 1. (bases 1 to 731)
AUTHORS Jantsuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
TITLE Kudrins, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.
JOURNAL Large-scale identification of ESTs involved in the interaction
COMMENT Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 08 row: F column: 21
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1. 731
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:3947"
/clone="OSUNEC08f21"
/issue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSUNEC"
/note="Vector: pBluescript II KS+; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"
ORIGIN
Query Match 21.6%; Score 419.2; DB 6; Length 731;
Best Local Similarity 73.5%; Pred. No. 2.8e-92;
Matches 535; Conservative 0; Mismatches 193; Indels 0; Gaps 0;
QY 931 CAGGAGAGAGGAGGATTTCAGGACAGAGGTTGATGATCAGAGAGTTGACCAAGGCAT 990
Db 1 CAGGAGAGAGGAGGATTTCAGGACAGAGGTTGATGATCAGAGAGTTGACCAAGGCAT 60
QY 991 CTGGTGTCTTGTGTTGTTTGAATTCATCCCGGTGCCAAAGATTGCTGTATGATTT 1050
Db 61 CTGGTGTCTTGTGTTGTTTGAATTCATCCCGGTGCCAAAGATTGCTGTATGATTT 120
QY 1051 GTTCTTAAACAATCTGAGCTTCACTCCATGAGCGAGGACGGCTTAAATGGAATG 1110
Db 121 GTTCTTAAACAATCTGAGCTTCACTCCATGAGCGAGGACGGCTTAAATGGAATG 180
QY 1111 AGCACAGATTGAAGATTGCTTGTGATCTGCTAAAGGACTTCTTATCTTATGAT 1170
Db 181 CCCACAGACTGAAGATTGCTTGTGAGCTCAAAAGGTTTATGCTTATCTTATGAT 240
QY 1171 TGCAATCCTTAAATCATTCACCGGATATCAAGGCTTAAACATTTATGATTTCAAG 1230
Db 241 TGCAATCCTTAAATCATTCACCGGATATCAAGGCTTAAACATTTATGATTTCAAG 300
QY 1231 TTTGAAGCTAAGGTTGCTGATTTTGTCTTGTGATGATGCTTGTGATTAACAACG 1290
Db 301 TTTGAAGCTAAGGTTGCTGATTTTGTCTTGTGATGATGCTTGTGATTAACAACG 360
QY 1291 GTATCAACAGTGTGATGAGAACTTTGGGACTTGTGCTCGGAATACGTCGAAGCG 1350
Db 361 GTTTCGCAAGAGTAAGGACATTTTGTGATATCAACAGAGTACGATCTTTCGGC 420
QY 1351 AAGCTCAGGAGAGGATGAGGTTTCTCAATTTGGCGCTTGTGCTTGTGAGCTATTA 1410
Db 421 AAGCTCAGGAGAGGATGAGGTTTCTCAATTTGGCGCTTGTGCTTGTGAGCTATTA 480
QY 1411 GAGAGTGAGCCGTTGATGCAACATGTCTATGATGATGACAGCTTATGATGAGG 1470
Db 481 GAGAGTGAGCCGTTGATGCAACATGTCTATGATGATGACAGCTTATGATGAGG 540
QY 1471 CGAACATTTGTTAACGAGATCTGAGCAAGAGACTTTAGAGGTTTATGCTGATG 1530
Db 541 AAGCTTTTACTGATGAGCAAGCTTGAATGATGATGATGATGATGATGATGATGAT 600
QY 1531 ATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1590
Db 601 CTGGGAGAGGATTTCAATCCCAATGATGATGATGATGATGATGATGATGATGATG 660
QY 1591 GTTTCGCAATTCAGCTGCGGAGAGCTCGCATGAGCCAGATTGCTGCTGTTAGAAG 1650

DB 661 GTACCGCATTCGCTGCTGCGCCACGACGAGCGAGTGTCCGGCTTGGAGGT 720

QY 1651 AATGTATC 1658

DB 721 GACGTGTC 728

RESULT 9
CNSOAKU 2734 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSIRPH52E04 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).

ACCESSION BX816903.1 GI:42469997

VERSION HTC; GSUT cDNA.

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2734)
Castelli,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpetti,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 2734)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/gsb/gsb?source=Arabidopsis.
Location/Qualifiers
1..2734
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSUTPH52E04"
/issue_type="Hormone Treated Callus"
/plasmid="PCWMSPORT_6"
1..2734
/gene="At1g70460"

ORIGIN

Query Match 21.5%; Score 417.6; DB 3; Length 2734;
Best Local Similarity 64.0%; Pred. No. 9.3e-92;
Matches 678; Conservative 0; Mismatches 354; Indels 28; Gaps 2;

QY 763 GTGTAGGCTTCCTCCAAAGCACTTTCACATACGAGAGCTAGAGCCACCAATGTT 822

DB 1306 GTGATGGAGAGTGTCACAAACATTTTCAATATGAAGACTAACGACATACAGAGGA 1365

QY 823 TTCTCGAGGCAACTTGTAGACAAAGCGGGTTCGTTCATCGTCACAAAGGTGTGTTG 882

DB 1366 TTTTCAAGCATTAACTATTGAGAGAGGTTTGTGTGTATTAAGGTAAATTA 1425

QY 883 CCTAGTGGAAAGAGTGTCTGTGAAGCAATTGAAAGTTGGAGATGTGTGAGGAGAGAG 942

DB 1426 AATGATGGAAACTTGTGTCTGTGTATGACAGCTTAAGTTGGTAGGAGCAAGGTACCCT 1485

QY 943 GAGTTTCAGGAGAGTTGAGATCATCATCAGAGTTTACACACAGGATCTGTGTCTTT 1002

DB 1486 GAGTTTAAAGCGAGGTGAGATTATTAAGCCGTGTTCATCATTCGCATTTGTGTCTTT 1545

QY 1003 GTTGTATTATGATCGCCGCGTCCAAAGATTGCTTGTATAGTTTGTCTTAACAC 1062

DB 1546 GTTGTATCTGATATGCGGATTCAGAGATTTGCTATCTATGAAATATTTCTTAACCA 1605

QY 1063 AATCTGAGCTTCACTTCATGAGCGAGGACGGCTTACATATGAAATGAGACACAGATTG 1122

DB 1606 ACATTTGAAACATCATTTGATGAGGAGGAGCGCCGTAATTGAATGGCTTAGAGAGTTC 1665

QY 1123 AGATTGTCTTGGATCTGTCTAAAGACTTCTTATCTTCATGAAATTTGCAATCTTAA 1182

DB 1666 AGAATTGCTATAGTTCCTGCAAGGTTTGGCGTATTATACAGAAAGACTGTACCCAAA 1725

QY 1183 ATCATTCACCGTATATCAAGGCTTCAACATATGATATGATTCAAGTTTGAAGCTAAG 1242

DB 1726 ATCATTCACAGGACATTAAGTCCGTAACATCTTGTGAGCATGAGTTGAAGCTCAG 1785

QY 1243 GTTGTGATTTTGTCTTGTGTAAGATTGCTTGTATCAACACGAGATATCAACAGT 1302

DB 1786 GTTGTGATCTTGTGACTTGGCAAACTCAATGATTCACACAAACTCATGTATCACTGCG 1845

QY 1303 GTGATGGGAACCTTTGGGTACTTGGCTCCGAAATAGCCTCAAGCGGAAAGCTCACGAG 1362

DB 1846 GTTATGGGAACCTTCGGGTACTTGGCACGAAATATCACAAAGTGAAGCTACATGAT 1905

QY 1363 AAGCTGACGTTTCTCATTTGGCGTTTGTCTTGTGAAGCTCATTTATCTGACGTCGACCC 1422

DB 1906 AGATCAAGATGTTTCTGTGTGGGTTTCTCTTAAGCTTATTAACAGCGGCAAACTT 1965

QY 1423 GTTGTATCCAAATGTCATATGATGAGACAGCTTAGTGACTGGGACGACCACTTCTT 1482

DB 1966 GTTATACCAATACCGCTTGGGAGAGAGATTGGTTGTAATGGCTCGCTCTGCTT 2025

QY 1483 AACGAGATCTGAGCAAGAGACTTTGAGGGTTAGCTGATGCAAAAGATGATATGAGG 1542

DB 2026 CACAAGCCATTGAGACCGGATTTTCACTGATCACTAGTTGATGATACGCGCTGAAAAGCAT 2085

QY 1543 TATGACAGAGAGAGATGCTGATGATGTTG-CTTGCTCTCGGCTTGTTCGCTATTC 1601

DB 2086 TATGTGGAGATGAAGTTTTCAGAAATGATGAAACAGCTCTGCTGTGTGTTAGCATTC 2145

QY 1602 AGCTGCCGAGAGCTTGCATGAGCCGATGTGTGGCGTTAGAAAGAAATGATCACT 1661

DB 2146 AGGTCCAAACGTCACGATATGTTTCAAGTTGTGAGACATTTGATGTAAGGGAGACAT 2205

QY 1662 GTGAGATCTTAAAGAGGATGAGACCAAGTCATGATGATATACAGCTCATACGAGG 1721

DB 2206 GGGAGATTCAGCAATGTGTAACAAAGTGAGCAAGCAAGT----- 2245

QY 1722 AAGCACGATTATGATCTGAGCGAGTATGATGAAGACATGAAGAGTTTGAAGAAATGCG 1781

DB 2246 -----GCTTATGACTCTGTGTCAGATATATATATACACCAAGAGTTTCAGGAAATGCG 2298

QY 1782 ACTTGAAGTCAAGATCAAGCCAGCGGATGATCACT 1821

DB 2299 ATTTGGTTTGAAGATGATGCTCGGATTCGCGGATGTACAGT 2338

RESULT 10
BG441204 692 bp mRNA linear EST 15-MAR-2001
LOCUS BG441204 Ead012C15f Gossypium arboreum 7-10 dpa fiber library
DEFINITION GA_Ead012C15f Gossypium arboreum cDNA clone GA_Ead012C15f, mRNA sequence.
ACCESSION BG441204 GI:13350856

KEYWORDS EST.
SOURCE Gossypium arboreum
ORGANISM Gossypium arboreum
REFERENCE Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS 1 (bases 1 to 692)
Henry, R.A., Frisch, D., Yu, Y., Main, D., Ramo, T., Simmons, J.,
TITLE An integrated analysis of the genetics, development, and evolution
JOURNAL of the cotton fiber
COMMENT Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 690.
Location/Qualifiers
1. 692
/organism="Gossypium arboreum"
/mol_type="mrna"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0012C15f"
/tissue_type="Fibers isolated from bolls harvested 7-10
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 21.3%; Score 413.2; DB 4; Length 692;
Best Local Similarity 75.4%; Pred. No. 8.4e-91;
Matches 514; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 739 CTTCCTCCACCGTCTCCAGGGCTGTCTAGGCTTCCAAAAGACATTTGACATGAG 798
DB 11 CTTCGGCTGCTACCTCGTATTTCTTAGGTTCTGAAAAGACATTTAGCTATGAA 70
QY 799 GAGCTAGTAGAGCCCAATGTTCTCCAGGCGAATCTGTAGGCAAGCGGGCTC 858
DB 71 GAATTAAG 130
QY 859 GGTACGTGCAAAAGGTGTGTCTAGTGGAGAAAGAGTGTGTGAGAGAGAGAG 918
DB 131 GGGTACGTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190
QY 919 GTTGGAGTGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
DB 191 GCTGAGAGTGGGCAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 250
QY 979 CACCAAGGAGATCTGATCTCTTGTGTATTCATCGCGGTGCAAAAGAGTCTT 1038
DB 251 CATCAAAAACATCTCGTCTATGTTGATGATCTGATCTTCTGGAGAAATAAGAT 310
QY 1039 GTCTAAGAGTGTCTCTTAAACAATCTGAGCTTCACTCCATGCGAGAGAG 1098
DB 311 GTTAAAGAGTGTCTTCAACAACACCTTGAGTTCACTTGAGAGAGAGAGAG 370
QY 1099 ACAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
DB 371 ACATGAGATTTGGCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
QY 1159 CTTCATGAAGATGAGATCTTAAATCATTCACCGAGATATCAAGGCTTCAACAT 1218
DB 431 CTTCATGAAGATGATGATCTTAAATCATTCACCGAGATATTAAGGCGCTAATAT 490
QY 1219 ATAGATTTCAAGTTGAAGCTAAGGTTGCTGATTTGCTTGTAAAGATGCTTCT 1278

DB 491 TTGATTTCAAGTTTGAAGCAAAAGTTGCTGATTTTGACATGAGCAAAATGCTTCGAT 550
QY 1279 ACAACAGCATGATATTAACACGCTGATGAGAACTTTGGTACTTGGCTCCGAAATAC 1338
DB 551 GTCAACAGCAGAGCTTCCACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 610
QY 1339 GCTGCAAGCGAG 1398
DB 611 GCTTCAAGTGAAG 670
QY 1399 GAGCTATTACTGAGCTGAC 1420
DB 671 GAGTTGATTACCGGTACAGAG 692

RESULT 11
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DEFINITION AV543493 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
ACCESSION CDNA clone RZ201f07F 3', mRNA sequence.
VERSION AV543493
KEYWORDS AV543493.1 GI:8714907
SOURCE EST
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 584)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
MEDLINE 20363093
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
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1. 584
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XhoI"

ORIGIN

Query Match 21.2%; Score 411.6; DB 1; Length 584;
Best Local Similarity 90.9%; Pred. No. 2e-90;
Matches 438; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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DB 584 ACTGGGACGACCATTTGCTTAAACGAGCATCTGAGCAAGAGAGAGAGAGAGAG 525
QY 1523 ATGCAAGATGAAATATGAGTATGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1582
DB 524 ATTCAAAGATGAGTATGAGTATGACAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 1583 CGGCTTGTGGCCATTCAGCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1642
DB 464 CGGCTTGTGTGGCCATTCAGCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 1643 TGAAGGAATATATCATCTGTCAGATCTTAAAGAGAGAGAGAGAGAGAGAGAG 1702

JOURNAL
Unpublished (2003)
Contact: Kazuki Moriguchi
Plant Genetics
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-981-6872
Fax: 81-55-981-6879
Email: kmoriguc@lab.nig.ac.jp
cDNA clone obtained from nuclear transportation trap system
encoding a protein similar to Oryza sativa (japonica
cultivar-group) putative receptor protein kinase PERK1.
Location/Qualifiers
1. .1084

FEATURES

source

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ORIGIN

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Best Local Similarity 69.3%; Pred. No. 1.3e-89;

Matches 587; Conservative 0; Mismatches 254; Indels 6; Gaps 2;

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1 CTTGACGAGAAAGGCCGACCAACATGAGTGGCCCAACAGATTAAGATTGCTTTGG 60
1137 ATCTGCTAAAGACTTTCTTATCTTCATGAAGATGCAATCCTAAATCATCACCCTGA 1196
61 AGCTCAAGAGGTTAGCTTATCTTCATGAAGATGCAATCCTAAATCATCACCCTGA 120
1197 TATCAAGCTTCAACATATGATGATTTCAAGTTGAAGCTAAGTTGCTGATTTGG 1256
121 TATTAAGCGCGCAACATTTCTTGAATTTAAGTTGAATTAAGTTGCTGATTTGG 180
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181 ACTTGCTAAGTTCACAGTGAATTAACATCATGTTTGCACAAAGTAATGGGCACTT 240
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241 TGAATATACACACAGAGTACGATCTTCTGCGAAGCTCCTAGAAATGATGCTT 300
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301 CTCTATGAGATGATGCTTCTTGAATTAATAGTGTGTGGCCAGTTGATCAAGTCA 360
1437 TGTCTATGATGATGACGCTTACTGATGCTGCGACAGCAATGCTTAAACGAGCATCTGA 1496
361 AACATATATGATATACAGCTGTTGACTGGGCAAGGCTTTACTGATGCAAGCACTTGA 420
1497 GCAAGAGACTTTGAGGTTTGAAGTGAACAAAGATGAATTAATGGGTAATGACAGAGGA 1556
421 GAATGTAACAGAGAGATTAAGATCTCCGCTTGGAGAGATTTCAATCCCAATGA 480
1557 GATGGCTCGCATGTTGCTGTGCTGGCTGTGTTGCGCATTCAGCTGCGCGCAGACC 1616
481 GATGGCGAGATGATGCTTGTGCTGAGCTGATGCTGAGCATTCGCTGCTGCTGCC 540
1617 TCGCATGAGCAATGTTGGTGGTGTAGAAAGAAATGATCACTGTCAGATCTTAAAGA 1676
541 ACCGATGAGCAAGGTTGCTGGGCTTTGGAAGGAGAGTGTCTTTGAGGATCTTATGA 600
1677 AGGAGATGAGCAAGCTCAAGCAATGATACAGCTCAAGAGAGAGCAACCATTTGA 1736
601 AGGTTGTTGGCTGTGACAGCCGCTATTTGATCTTAC--AGACGCTCTGACTATGA 657
1737 CTGAGCGCATCAATGAGACATGAAGATTAGAAATGCACTTGGAACTCAGA 1796

Db 658 TTCTGGCCATATCAACAGAGCATGAAGAAGTTCAAGAAATGAGCTTT--ACCAACA 714
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Qy 1857 TTCAACAGAGAGGCGCAACACCAACAGCAATGAGATGAGGATTAAGAAACCG 1916
Db 775 ATCAACAGAGAGGCGCAACCAACAGCAATGAGATGAGGATTAAGAAACCG 834
Qy 1917 TCAAGGT 1923
Db 835 CTACAGT 841

RESULT 14
CP436655
LOCUS EST673000 normalized cDNA library of onion Allium cepa cDNA clone
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 789)
Havey,M.J., Cheung,F., Van Aken,S., Uteback,T. and Town,C.D.
Expressed Sequence Tags from a normalized library of mixed onion
tissues (Allium cepa)
Unpublished (2003)
Contact: Havey MJ
Department of Horticulture
USDA-ARS and University of Wisconsin
1575 Linden Drive, Madison, WI 53706, USA
Tel: 608-262-1830
Fax: 608-262-4743
Email: mjhavey@facstaff.wisc.edu
TIGR sequence name ACCK26TR. For more information:
http://haveylab.hort.wisc.edu
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES

source

Location/Qualifiers
1. .789
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synthesize the library. Normalization to enrich for
low-copy transcripts was performed by proprietary
techniques of Invitrogen."

ORIGIN

Query Match 20.9%; Score 405.6; DB 7; Length 789;
Best Local Similarity 69.7%; Pred. No. 6.5e-89;

Matches 549; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

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Qy 838 TTGTTGAGCAAGCGGTTGGTTCAGTGCACAAAGGTGTGTTGCTAATGGAAAGAA 897
Db 62 CTTCCTGGCGAAGGTGATTTGATATGTGACAAAGAGTACTTCCAAACGGTAAGAA 121


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Db      611 GCAAGCCGCTGCGCCACGATGAGTCAAGTGTTCGGGCCCTTGAAGGTGACGTGTCTTGG 670
QY      1663 TCAGATCTTAAAGGAGATGAGACCAGTCAAGCAATGTATACGCTCATACGAGGA 1722
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Db      671 GAAGATCTTAAAGAGGTGTTCGGCCCTGSCCATAGCCGCTTCTTTGATGTAC--AGC 727
QY      1723 AGCACCAGTTATGACTCGAGCCAGTACATGAAGACATGAAGATTAGAAATGSCA 1782
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Db      728 AGTTCGACTACGATTCTGACACAGTATAAGAGGACATGAAGAAAGTTGAGAGATGGCT 787
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Db      788 TTACGACGACGACTACA 806

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 Job time : 4172 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 10:58:35 ; Search time 5549 Seconds

(without alignments)
16567.161 Million cell updates/sec

Title: US-10-069-304-1
Perfect score: 1944

Sequence: 1 atgctctgcgcgcgcgtctcc.....atagctgacctctctcttaa 1944

Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

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2: gb_hig: *
3: gb_in: *
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7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
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12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1944	100.0	1944	6	AX088876 Sequence
2	1944	100.0	1944	6	AX825703 Sequence
3	1944	100.0	2189	6	AX825705 Sequence
4	1944	100.0	2189	8	AY028699 Brassica
5	66	3.4	668	8	AY536856 Arabidops
6	66	3.4	1959	6	AX825738 Sequence
7	66	3.4	1959	8	BT008400 Arabidops
8	66	3.4	1959	8	BT008409 Arabidops
9	66	3.4	2098	8	AY128792 Arabidops
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11	66	3.4	2188	8	AY059901 Arabidops
12	66	3.4	2190	8	AY093065 Arabidops
13	66	3.4	2257	8	AF370509 Arabidops
14	66	3.4	2257	8	AB020746 Arabidops
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18	26	1.3	47428	6	AX059540 Sequence
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20	1.3	145453	8	AC012477	AC012477 Genomic S
21	1.3	183147	8	AC012392	AC012392 Genomic S
22	1.3	199987	8	ATCHR1V15	ATCHR1V15
23	1.2	898	8	AK109201	AK109201 Oryza sat
24	1.2	1389	6	AK654306	AK654306 Sequence
25	1.2	1922	8	AK070323	AK070323 Oryza sat
26	1.2	147516	8	AP004622	AP004622 Oryza sat
27	1.2	256	11	G12716	G12716 SMS2029 Br
28	1.2	450	8	AF213398	AF213398 Ovis arie
29	1.2	650	8	AY536855	AY536855 Arabidops
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32	1.2	897	6	AX546187	AX546187 Sequence
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34	1.2	1281	6	AX546185	AX546185 Sequence
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36	1.2	2016	9	HSU19348	HSU19348 Human activ
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38	1.2	3407	8	AY064019	AY064019 Arabidops
39	1.2	3677	9	HSMB08933	HSMB08933
40	1.2	4406	4	AY543631	AY543631 Homo sapi
41	1.2	4419	4	AB118945	AB118945 Canis fam
42	1.2	4443	6	CQ727681	CQ727681 Sequence
43	1.2	4456	9	HSMBETPRO	HSMBETPRO
44	1.2	4620	6	CQ776403	CQ776403 Sequence
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46	1.2	4626	6	196185	196185 Sequence 22
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49	1.2	4823	4	AB112434	AB112434 Bos tauru
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52	1.2	73840	8	AB007644	AB007644 Arabidops
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55	1.2	121659	8	AC137001	AC137001 Oryza sat
56	1.2	137416	2	AC147842	AC147842 Ovis arie
57	1.2	141415	4	AC087214	AC087214 Papio anu
58	1.2	150635	9	AC130186	AC130186 Ateles
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65	1.2	197836	4	AC090032	AC090032 Canis fam
66	1.2	203696	4	AC087860	AC087860 Bos tauru
67	1.2	206830	2	AC148187	AC148187 Saimiri b
68	1.2	208707	9	AC084729	AC084729 Papio anu
69	1.2	300350	1	AP006574	AP006574 Gloeobact
70	1.2	349907	1	BX571874	BX571874 Phototrab
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72	1.1	127576	5	OSJN00296	OSJN00296 Danio rer
73	1.1	141099	8	AC139526	AC139526 Oryza sat
74	1.1	152676	8	OSJN00078	OSJN00078 Medicago
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76	1.1	193421	9	AC107294	AC107294 Oryza sat
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78	1.1	861	8	AF016274	AF016274 Trilicium
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82	1.1	1857	8	BT012797	BT012797 Nicotiana t
83	1.1	1949	6	AX054443	AX054443 Lycopersi
84	1.1	2046	6	AK000342	AK000342 Homo sapi
85	1.1	2048	6	AX405737	AX405737 Sequence
86	1.1	2050	9	AY274811	AY274811 Homo sapi
87	1.1	2196	6	AX088879	AX088879 Sequence
88	1.1	2196	6	AX825709	AX825709 Sequence
89	1.1	2231	6	AX088878	AX088878 Sequence
90	1.1	2231	6	AX825708	AX825708 Sequence
91	1.1	2313	6	AX120541	AX120541 Oryza sat
92	1.1	2465	8	U00889	U00889 Hansenula p

93	21	1.1	2817	9	AK131385	Homo sapi	166	21	1.1	240340	2	AC095354	AC095354 Rattus no
94	21	1.1	2837	8	AY059769	Arabidops	167	21	1.1	242559	2	AC098256	AC098256 Rattus no
95	21	1.1	2891	6	AX105698	Sequence	168	21	1.1	243005	2	AC134740	AC134740 Rattus no
96	21	1.1	3120	8	AF199021	Chlamydom	169	21	1.1	245422	2	AC106225	AC106225 Rattus no
97	21	1.1	3764	9	HSMB02129	Al137938 Homo sapi	170	21	1.1	255991	2	AC106225	AC106225 Rattus no
98	21	1.1	3842	6	CO841723	Sequence	171	21	1.1	262581	2	AC116220	AC116220 Rattus no
99	21	1.1	4237	9	AK124775	Homo sapi	172	21	1.1	266049	2	AC103504	AC103504 Rattus no
100	21	1.1	5970	5	HSMB06302	BSX31600 Homo sapi	173	21	1.1	274964	2	AC130982	AC130982 Rattus no
101	21	1.1	7305	8	AL621356	BSX31366 Tetradon	174	21	1.1	287501	2	AC098561	AC098561 Rattus no
102	21	1.1	10528	1	PTGWIN62B	X59955 P. trichocor	175	21	1.1	340493	10	EX883044	EX883044 Rattus no
103	21	1.1	15514	8	AE008644	AE008644 Rickettsi	176	21	1.1	349938	6	AX647882	AX647882 Rattus no
104	21	1.1	17871	6	RR1293314	Al2993314 Rickettsi	177	20	1.0	150	8	CR378280	CR378280 Rattus no
105	21	1.1	17971	6	AX059525	Sequence	178	20	1.0	213	6	CO466837	CO466837 Rattus no
106	21	1.1	27960	6	AX059506	Sequence	179	20	1.0	290	8	AY225995	AY225995 Rattus no
107	21	1.1	40740	8	AC027349	Homo sapi	180	20	1.0	334	3	AY380130	AY380130 Rattus no
108	21	1.1	80472	8	AC007945	Genomic's	181	20	1.0	339	11	BY090932	BY090932 Rattus no
109	21	1.1	82010	8	AB023042	AB023042 Arabidops	182	20	1.0	478	3	AY12605	AY12605 Rattus no
110	21	1.1	82532	8	AC006219	Continuation (5 of	183	20	1.0	500	9	AY520144	AY520144 Rattus no
111	21	1.1	86455	2	AL137076	Human DNA	184	20	1.0	506	8	CR377590	CR377590 Rattus no
112	21	1.1	89259	9	AL137076	Arabidops	185	20	1.0	506	9	AY520143	AY520143 Rattus no
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114	21	1.1	99923	8	FS08	Arabidops	187	20	1.0	586	11	G88001	G88001 Rattus no
115	21	1.1	108277	8	AP006108	Lotus cor	188	20	1.0	601	11	BY191997	BY191997 Rattus no
116	21	1.1	110000	2	AC115142	Rattus no	189	20	1.0	609	6	AR374755	AR374755 Rattus no
117	21	1.1	110000	2	AC132992	Continuation (3 of	190	20	1.0	657	6	TOBCELPD	TOBCELPD Rattus no
118	21	1.1	110000	8	CR382131	Continuation (35 of	191	20	1.0	680	8	AK066856	AK066856 Rattus no
119	21	1.1	111780	2	AC137670	Medicago	192	20	1.0	687	8	EMT85402	EMT85402 Rattus no
120	21	1.1	116780	8	AC146237	Medicago	193	20	1.0	690	14	HYMOVIR1A1	HYMOVIR1A1 Rattus no
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122	21	1.1	131142	9	AC073156	AC073156 Homo sapi	195	20	1.0	773	11	BY026331	BY026331 Rattus no
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125	21	1.1	13410	2	AC147001	Arabidops	198	20	1.0	896	9	AY520140	AY520140 Rattus no
126	21	1.1	142937	8	AC005171	Arabidops	199	20	1.0	922	6	AP506202	AP506202 Rattus no
127	21	1.1	146742	2	AC139916	Rattus no	200	20	1.0	922	6	AX662314	AX662314 Rattus no
128	21	1.1	149089	8	AP003991	Oryza sat	201	20	1.0	1002	6	AK058665	AK058665 Rattus no
129	21	1.1	151265	8	AP003991	Rattus no	202	20	1.0	1063	8	AK099480	AK099480 Rattus no
130	21	1.1	156678	2	AC149449	Papio anu	203	20	1.0	1153	8	AK118297	AK118297 Rattus no
131	21	1.1	157583	5	BSX71951	Zebrafish	204	20	1.0	1212	6	AX655977	AX655977 Rattus no
132	21	1.1	164781	9	AC092440	Homo sapi	205	20	1.0	1236	6	CR352526	CR352526 Rattus no
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134	21	1.1	171175	2	AC135507	Homo sapi	207	20	1.0	1261	5	CR352526	CR352526 Rattus no
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136	21	1.1	177434	2	AC148954	Otolemur	209	20	1.0	1509	6	AB026543	AB026543 Rattus no
137	21	1.1	178119	9	AC116036	Homo sapi	210	20	1.0	1540	10	AF420251	AF420251 Rattus no
138	21	1.1	182444	2	AC027188	Homo sapi	211	20	1.0	1701	6	CO412052	CO412052 Rattus no
139	21	1.1	187746	2	AC087123	Mus muscu	212	20	1.0	1772	5	VCPPHEROPH	VCPPHEROPH Rattus no
140	21	1.1	194431	2	AC120280	Rattus no	213	20	1.0	1800	8	AT006883514	AT006883514 Rattus no
141	21	1.1	194866	2	AC142140	Rattus no	214	20	1.0	1830	9	BC065472	BC065472 Rattus no
142	21	1.1	195987	10	AC125337	Mus muscu	215	20	1.0	1849	5	AX088882	AX088882 Rattus no
143	21	1.1	197411	10	AC135961	Mus muscu	216	20	1.0	1902	6	AX825712	AX825712 Rattus no
144	21	1.1	198392	10	AL603745	Mouse DNA	217	20	1.0	1939	6	AX088881	AX088881 Rattus no
145	21	1.1	200635	2	AC111613	Rattus no	218	20	1.0	1939	6	AX825711	AX825711 Rattus no
146	21	1.1	201078	2	AC122220	Mus muscu	219	20	1.0	1939	6	AX825711	AX825711 Rattus no
147	21	1.1	202612	2	AC148952	Otolemur	220	20	1.0	1985	8	AK105670	AK105670 Rattus no
148	21	1.1	206506	2	AC025585	Mus muscu	221	20	1.0	1990	8	AB078412	AB078412 Rattus no
149	21	1.1	206973	2	AC130594	Rattus no	222	20	1.0	2042	5	AK105266	AK105266 Rattus no
150	21	1.1	208694	2	AC130867	Rattus no	223	20	1.0	2056	5	BC067334	BC067334 Rattus no
151	21	1.1	210000	2	AC006295	Homo sapi	224	20	1.0	2064	5	BC047852	BC047852 Rattus no
152	21	1.1	215916	10	AL662922	Mouse DNA	225	20	1.0	2225	8	STU306627	STU306627 Rattus no
153	21	1.1	217622	2	AC126569	Rattus no	226	20	1.0	2237	8	STU306629	STU306629 Rattus no
154	21	1.1	220713	10	AC025047	Rattus no	227	20	1.0	2268	6	Q0842119	Q0842119 Rattus no
155	21	1.1	221585	2	AC097412	Rattus no	228	20	1.0	2272	10	AY033645	AY033645 Rattus no
156	21	1.1	222880	6	AX647883	Sequence	229	20	1.0	2755	6	AX305505	AX305505 Rattus no
157	21	1.1	226601	10	AC095762	Sequence	230	20	1.0				
158	21	1.1	227897	2	AC112863	Rattus no	231	20	1.0				
159	21	1.1	228492	10	AC113962	Rattus no	232	20	1.0				
160	21	1.1	232516	2	AC132058	Rattus no	233	20	1.0				
161	21	1.1	233405	2	AC108828	Mus muscu	234	20	1.0				
162	21	1.1	234746	10	AC126733	Rattus no	235	20	1.0				
163	21	1.1	235343	2	CNS080CAS	Mus muscu	236	20	1.0				
164	21	1.1	237997	2	AC121745	Rattus no	237	20	1.0				
165	21	1.1	237997	2	AC093989	Rattus no	238	20	1.0				

C 239	20	1.0	2755	10	MMU17698	U17698 Mus musculu	C 312	20	1.0	110000	2	BX324168_4	Continuation (5 of
C 240	20	1.0	2840	5	BC068922	BC068922 Xenopus 1	C 313	20	1.0	110000	8	CR380958_12	Continuation (13 o
C 241	20	1.0	2869	5	BD160752	BD160752 Method of	C 314	20	1.0	110000	8	CR382132_15	Continuation (16 o
C 242	20	1.0	2918	5	AF224315	AF224315 Gallus gae	C 315	20	1.0	110000	8	CR382132_22	Continuation (23 o
C 243	20	1.0	2962	10	BC079642	BC079642 Mus muscu	C 316	20	1.0	110000	8	AC145127_12	Continuation (13 o
C 244	20	1.0	3043	8	SPDASGEN	X14488 S.pombe ade	C 317	20	1.0	111338	8	ATF1612	AL162459 Arabidops
C 245	20	1.0	3043	8	YSPADE6	M37264 S.pombe pho	C 318	20	1.0	1117046	2	AC135600	AC135600 Oryza sat
C 246	20	1.0	3046	6	AK747634	AK747624 Sequence	C 319	20	1.0	118045	2	AC138014	AC138014 Oryza sat
C 247	20	1.0	3046	6	AK092602	AK092602 Homo sapi	C 320	20	1.0	118101	2	AC091665	AC091665 Oryza sat
C 248	20	1.0	3097	6	BD266932	BD266932 Compositi	C 321	20	1.0	118951	9	AC068274	AC068274 Homo sapi
C 249	20	1.0	3097	6	AR201531	AR201531 Sequence	C 322	20	1.0	119270	2	AY508219	AY508219 Medicago
C 250	20	1.0	3199	3	AB046873	AB046873 Halocynch	C 323	20	1.0	120476	2	AC130375	AC130375 Homo sapi
C 251	20	1.0	3234	5	BC073490	BC073490 Xenopus 1	C 324	20	1.0	120665	10	AL929140	AL929140 Mouse DNA
C 252	20	1.0	3371	10	BC004557	BC004557 Mus muscu	C 325	20	1.0	121309	9	AC026798	AC026798 Homo sapi
C 253	20	1.0	3431	14	STU57047	U57047 Elm mottle	C 326	20	1.0	122390	2	AC135918	AC135918 Oryza sat
C 254	20	1.0	3475	3	AF303661	AF303661 Halocynch	C 327	20	1.0	122769	2	AC103371	AC103371 Mus muscu
C 255	20	1.0	3543	6	AX151655	AX151655 Sequence	C 328	20	1.0	123123	2	AC016610	AC016610 Homo sapi
C 256	20	1.0	3753	3	AY353563	AY353563 Anopheles	C 329	20	1.0	124191	9	AC005153	AC005153 Homo sapi
C 257	20	1.0	4005	3	HSMB07100	BX640951 Homo sapi	C 330	20	1.0	124204	8	CNS08CCQ	AL954152 Oryza sat
C 258	20	1.0	4666	9	AK128724	AK128724 Homo sapi	C 331	20	1.0	124536	2	AC149107	AC149107 Papio anu
C 259	20	1.0	4698	10	AB033168	AB033168 Homo sapi	C 332	20	1.0	125153	4	CNS08CC8	AL928778 Oryza sat
C 260	20	1.0	4705	9	AB020707	AB020707 Homo sapi	C 333	20	1.0	125661	9	AC087731	AC087731 Felis cat
C 261	20	1.0	4769	9	AF454702	AF454702 Homo sapi	C 334	20	1.0	125856	8	HS1187M17	AL121891 Human DNA
C 262	20	1.0	4823	9	BC050283	BC050283 Homo sapi	C 335	20	1.0	125909	8	AP005200	AP005200 Oryza sat
C 263	20	1.0	5720	6	AR374718	AR374718 Sequence	C 336	20	1.0	126447	9	OSJN00189	AL662985 Oryza sat
C 264	20	1.0	5868	6	AX026122	AX026122 Sequence	C 337	20	1.0	126447	9	AL592549	AL592549 Human DNA
C 265	20	1.0	6034	8	AF205407	AF205407 Neurospor	C 338	20	1.0	129302	8	AC133778	AC133778 Oryza sat
C 266	20	1.0	6316	6	AF179442	AF179442 Lycopersi	C 339	20	1.0	130740	8	AC144343	AC144343 Medicago
C 267	20	1.0	10302	1	ABE004757	ABE004757 Pseudomon	C 340	20	1.0	131414	2	AC148088	AC148088 Homo sapi
C 268	20	1.0	11608	1	AB24593	AB24593 Oryza sat	C 341	20	1.0	131531	8	CNS09SC2	AL606654 Oryza sat
C 269	20	1.0	13701	8	AB124593	AB124593 Drosophil	C 342	20	1.0	132854	9	OSJN00100	HS20N2
C 270	20	1.0	16975	2	AC019867	AC019867 Drosophil	C 343	20	1.0	133574	8	CNS08CAY	AL031330 Human DNA
C 271	20	1.0	18653	2	AC019887	AC019887 Drosophil	C 344	20	1.0	134414	8	OSJN00200	AL844875 Oryza sat
C 272	20	1.0	32218	3	AF038615	AF038615 Caenorhab	C 345	20	1.0	135940	8	AC116603	AL662999 Oryza sat
C 273	20	1.0	36556	3	BX908402	BX908402 Human DNA	C 346	20	1.0	137568	8	AC093178	AC116603 Oryza sat
C 274	20	1.0	38822	3	CBRG01A11	CBRG01A11 Caenorhab	C 347	20	1.0	138938	2	AC010111	AC093178 Oryza sat
C 275	20	1.0	41100	6	AX192230	AX192230 Sequence	C 348	20	1.0	139014	8	AF004233	AC010111 Drosophil
C 276	20	1.0	43070	8	SPCC122	SPCC122 Sequence	C 349	20	1.0	139208	2	CR391998	AP004233 Oryza sat
C 277	20	1.0	43709	8	BX649635	BX649635 Human DNA	C 350	20	1.0	139971	8	OSJN00294	CR391998 Oryza sat
C 278	20	1.0	49269	8	AC135499	AC135499 Oryza sat	C 351	20	1.0	139971	8	AC007425	AC007425 Homo sapi
C 279	20	1.0	61843	8	NC1586	AL153822 Neurospor	C 352	20	1.0	140738	2	AC116517	AC007425 Homo sapi
C 280	20	1.0	65074	2	AC118706	AC118706 Mus muscu	C 353	20	1.0	142134	8	AP005632	AC116517 Homo sapi
C 281	20	1.0	65172	2	AC101325	AC101325 Mus muscu	C 354	20	1.0	142134	8	AP003266	AP005632 Oryza sat
C 282	20	1.0	67078	2	AC100827	AC100827 Mus muscu	C 355	20	1.0	142239	8	AL589843	AP003266 Oryza sat
C 283	20	1.0	68003	2	BX323853	BX323853 Homo sapi	C 356	20	1.0	142527	2	AC142159	AL589843 Human DNA
C 284	20	1.0	68003	2	AP005969	AP005969 Oryza sat	C 357	20	1.0	143220	2	AC015470	AC142159 Homo sapi
C 285	20	1.0	7305	8	NCB13A5	AL513465 Neurospor	C 358	20	1.0	143416	2	ATF4P12	AC015470 Homo sapi
C 286	20	1.0	73684	9	AC010300	AC010300 Homo sapi	C 359	20	1.0	144628	8	ATF4P12	ATF4P12 Homo sapi
C 287	20	1.0	73684	9	AC147804	AC147804 Oryza sat	C 360	20	1.0	144738	2	AC112668	AL132668 Mus muscu
C 288	20	1.0	77273	8	AB022223	AB022223 Arabidops	C 361	20	1.0	145100	8	AP004727	AC112668 Oryza sat
C 289	20	1.0	80561	8	AC073555	AC073555 Arabidops	C 362	20	1.0	145107	8	AP004727	AP004727 Oryza sat
C 290	20	1.0	80561	8	AC128660	AC128660 Medicago	C 363	20	1.0	145526	8	AC079179	AP004727 Oryza sat
C 291	20	1.0	80716	2	AP005658	AP005658 Oryza sat	C 364	20	1.0	145526	8	CNS08CBA	AC079179 Oryza sat
C 292	20	1.0	80896	8	AC006135	AC006135 Arabidops	C 365	20	1.0	147164	2	AP003834	AL731786 Oryza sat
C 293	20	1.0	82356	8	AB013394	AB013394 Arabidops	C 366	20	1.0	147198	8	AF466203	AP003834 Oryza sat
C 294	20	1.0	85661	8	AC005882	AC005882 Arabidops	C 367	20	1.0	147344	8	AC091532	AF466203 Zea mays
C 295	20	1.0	87394	8	AC145780	AC145780 Oryza sat	C 368	20	1.0	147486	10	AL670276	AC091532 Oryza sat
C 296	20	1.0	88044	8	AC145780	AC145780 Oryza sat	C 369	20	1.0	148179	9	AC093677	AL670276 Mouse DNA
C 297	20	1.0	89464	2	AC138543	AC138543 Magnapor	C 370	20	1.0	148381	8	AP003253	AC093677 Homo sapi
C 298	20	1.0	90596	2	TI5B16	AF104919 Arabidops	C 371	20	1.0	148802	8	AP003207	AP003253 Oryza sat
C 299	20	1.0	91470	2	AC138708	AC138708 Homo sapi	C 372	20	1.0	149181	8	OSJN00251	AP003207 Oryza sat
C 300	20	1.0	91966	2	AC138708	AC138708 Homo sapi	C 373	20	1.0	149318	2	AC091554	AL731602 Oryza sat
C 301	20	1.0	92861	8	AC006439	AC006439 Arabidops	C 374	20	1.0	149414	9	BX957226	AC091554 Oryza sat
C 302	20	1.0	96205	8	AP006176	AP006176 Oryza sat	C 375	20	1.0	149457	8	AP004193	BX957226 Homo sapi
C 303	20	1.0	96700	8	HS28010	AL031316 Human DNA	C 376	20	1.0	149457	10	AC123235	AP004193 Oryza sat
C 304	20	1.0	97700	8	AC012563	AC012563 Arabidops	C 377	20	1.0	149654	8	AC080019	AC123235 Oryza sat
C 305	20	1.0	101966	8	AF448416	AF448416 Zea mays	C 378	20	1.0	150128	8	AP005409	AC080019 Homo sapi
C 306	20	1.0	106186	8	AP006059	AP006059 Oryza sat	C 379	20	1.0	150552	8	AC148058	AP005409 Oryza sat
C 307	20	1.0	107109	8	HSJ0781B1	AL118522 Human DNA	C 380	20	1.0	151547	8	AP003312	AC148058 Oryza sat
C 308	20	1.0	107120	2	AC091831	AL513122 Human DNA	C 381	20	1.0	152192	8	AC141346	AP003312 Oryza sat
C 309	20	1.0	108930	2	AL513122	Continuation (5 of	C 382	20	1.0	152702	8	AP005162	AC141346 Oryza sat
C 310	20	1.0	108930	2	AL513122	Continuation (5 of	C 383	20	1.0	152737	8	AC092931	AC092931 Homo sapi
C 311	20	1.0	110000	2	BX324168_4	Continuation (5 of	C 384	20	1.0	153939	2	AC110906	AL10906 Mus muscu

385	C	458	20	1.0	183467	2	AC133154	AC133154	Mus muscu
386	1.0	183917	20	1.0	183917	2	AC093795	AC093795	AC093795 Homo sapi
C 387	20	1.0	185048	20	1.0	185048	10	AC099631	AC099631 Mus muscu
C 388	20	1.0	185320	20	1.0	185320	8	AP006101	AP006101 Lotu
C 389	20	1.0	186333	20	1.0	186333	8	AP005689	AP005689 Oryza sat
C 390	20	1.0	186719	20	1.0	186719	2	AC147574	AC147574 Homo sapi
C 391	20	1.0	187471	20	1.0	187471	8	AP004232	AP004232 Oryza sat
C 392	20	1.0	187605	20	1.0	187605	2	AC141810	AC141810 Apis mell
C 393	20	1.0	187927	20	1.0	187927	2	AC147924	AC147924 Xenopus t
C 394	20	1.0	188520	20	1.0	188520	2	AC109298	AC109298 Mus muscu
C 395	20	1.0	189705	20	1.0	189705	10	AC131088	AC131088 Mus muscu
C 396	20	1.0	189917	20	1.0	189917	2	AC120606	AC120606 Rattus no
C 397	20	1.0	190679	20	1.0	190679	2	AC147747	AC147747 Homo sapi
C 398	20	1.0	190680	20	1.0	190680	9	AC147575	AC147575 Homo sapi
C 399	20	1.0	191918	20	1.0	191918	2	AC026484	AC026484 Homo sapi
C 400	20	1.0	193168	20	1.0	193168	2	AP001194	AP001194 Homo sapi
C 401	20	1.0	193625	20	1.0	193625	2	AP001194	AP001194 Homo sapi
C 402	20	1.0	194068	20	1.0	194068	2	CR391971	CR391971 Dantio rer
C 403	20	1.0	194476	20	1.0	194476	2	AC115327	AC115327 Rattus no
C 404	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 405	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 406	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 407	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 408	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 409	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 410	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 411	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 412	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 413	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 414	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 415	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 416	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 417	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 418	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 419	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 420	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 421	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 422	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 423	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 424	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 425	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 426	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 427	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 428	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 429	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 430	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 431	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 432	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 433	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 434	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 435	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 436	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 437	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 438	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 439	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 440	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 441	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 442	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 443	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 444	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 445	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 446	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 447	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 448	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 449	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 450	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 451	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 452	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 453	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 454	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 455	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 456	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi
C 457	20	1.0	194599	20	1.0	194599	2	AC147745	AC147745 Homo sapi

531	20	1.0	226001	8	AF391808	Zea mays	604	19	1.0	201	11	BV207405	BV207405 sqmm22340
532	20	1.0	226303	2	AC133489	Mus muscu	605	19	1.0	201	11	BV207408	BV207408 sqmm22341
533	20	1.0	227681	2	AC110885	Mus muscu	606	19	1.0	211	5	CHKMET	D38404 Chicken mri
534	20	1.0	228931	2	AC131355	Rattus no	607	19	1.0	215	12	AR463529	AR463529 Synthetic
535	20	1.0	229292	2	AC128826	Rattus no	608	19	1.0	235	8	CR354473	CR354473 Pinus pin
536	20	1.0	230449	2	BX601648	Danio rer	609	19	1.0	245	8	CR377681	CR377681 Pinus pin
537	20	1.0	230672	10	AL772397	Mouse DNA	610	19	1.0	250	8	CR377447	CR377447 Pinus pin
538	20	1.0	231989	10	AL772397	Mouse DNA	611	19	1.0	250	11	BV088106	BV088106 Pinus pin
539	20	1.0	233993	2	AC128993	Rattus no	612	19	1.0	292	6	AX363361	AX363361 Sequence
540	20	1.0	234580	2	AC130855	Rattus no	613	19	1.0	302	3	AY186678	AY186678 Cancer ma
541	20	1.0	234675	2	AC097407	Rattus no	614	19	1.0	333	6	AR147989	AR147989 Sequence 22
542	20	1.0	236096	2	AC094782	Rattus no	615	19	1.0	358	6	AR219713	AR219713 Sequence
543	20	1.0	237630	2	AC106665	Rattus no	616	19	1.0	358	6	AR350811	AR350811 Sequence
544	20	1.0	238372	2	AC096926	Rattus no	617	19	1.0	358	6	AR433187	AR433187 Sequence
545	20	1.0	241281	10	AC087063	Mus muscu	618	19	1.0	358	6	AX116831	AX116831 Sequence
546	20	1.0	241522	2	AC137599	Oryza sat	619	19	1.0	358	6	BD084364	BD084364 Compositi
547	20	1.0	241543	2	AC099472	Rattus no	620	19	1.0	437	6	AX886919	AX886919 Sequence
548	20	1.0	241887	2	AC094044	Rattus no	621	19	1.0	437	6	BD026529	BD026529 Sequence
549	20	1.0	245548	2	AC112899	Rattus no	622	19	1.0	437	6	BT006546	BT006546 Arabidops
550	20	1.0	246577	2	AC136124	Rattus no	623	19	1.0	462	8	CO069746	CO069746 Sequence
551	20	1.0	246805	2	AC098750	Rattus no	624	19	1.0	462	8	CO069746	CO069746 Sequence
552	20	1.0	247248	2	AC106695	Rattus no	625	19	1.0	463	6	CO096999	CO096999 Sequence
553	20	1.0	247575	2	AC133047	Rattus no	626	19	1.0	463	6	CO135808	CO135808 Sequence
554	20	1.0	247588	10	AC114512	Rattus no	627	19	1.0	463	6	CO174113	CO174113 Sequence
555	20	1.0	248059	2	AC113756	Rattus no	628	19	1.0	463	6	CO219104	CO219104 Sequence
556	20	1.0	248529	2	AC097592	Rattus no	629	19	1.0	463	6	CO257654	CO257654 Sequence
557	20	1.0	249274	2	AC123229	Rattus no	630	19	1.0	463	6	CO294911	CO294911 Sequence
558	20	1.0	249632	2	AC096927	Rattus no	631	19	1.0	463	6	CO331560	CO331560 Sequence
559	20	1.0	249961	2	AC130081	Rattus no	632	19	1.0	479	11	AU026793	AU026793 Rattus no
560	20	1.0	251533	2	AC125364	Rattus no	633	19	1.0	524	8	AB108371	AB108371 Phleum pr
561	20	1.0	251710	2	AC117065	Rattus no	634	19	1.0	524	8	CR354486	CR354486 Pinus pin
562	20	1.0	251773	2	AC079129	Mus muscu	635	19	1.0	531	6	CO078970	CO078970 Sequence
563	20	1.0	251872	2	AC125998	Rattus no	636	19	1.0	531	6	CO110189	CO110189 Sequence
564	20	1.0	252889	2	AC120743	Rattus no	637	19	1.0	531	6	CO148898	CO148898 Sequence
565	20	1.0	253184	2	AC137219	Rattus no	638	19	1.0	531	6	CO184031	CO184031 Sequence
566	20	1.0	253328	2	AC130341	Homo sapi	639	19	1.0	531	6	CO232171	CO232171 Sequence
567	20	1.0	255446	2	AC095420	Rattus no	640	19	1.0	531	6	CO270276	CO270276 Sequence
568	20	1.0	255818	2	AC145871	Pan trogl	641	19	1.0	531	6	CO307485	CO307485 Sequence
569	20	1.0	256476	10	AC126940	Mus muscu	642	19	1.0	547	8	CR377638	CR377638 Pinus pin
570	20	1.0	259158	2	AC099470	Rattus no	643	19	1.0	547	8	CR377638	CR377638 Pinus pin
571	20	1.0	260517	2	AC111318	Rattus no	644	19	1.0	554	11	G94971	G94971 S208P6791F
572	20	1.0	260517	2	AC097621	Rattus no	645	19	1.0	586	11	G63087	G63087 SHGC-140687
573	20	1.0	261056	2	AC119075	Rattus no	646	19	1.0	586	11	G63087	G63087 SHGC-140687
574	20	1.0	261056	2	AC119075	Rattus no	647	19	1.0	586	11	G63087	G63087 SHGC-140687
575	20	1.0	261749	2	AC131472	Rattus no	648	19	1.0	586	11	G63087	G63087 SHGC-140687
576	20	1.0	268151	2	AC111391	Rattus no	649	19	1.0	586	11	G63087	G63087 SHGC-140687
577	20	1.0	270068	2	AC113213	Rattus no	650	19	1.0	586	11	G63087	G63087 SHGC-140687
578	20	1.0	270962	2	AC149067	Mus muscu	651	19	1.0	586	11	G63087	G63087 SHGC-140687
579	20	1.0	271101	2	AC132376	Mus muscu	652	19	1.0	586	11	G63087	G63087 SHGC-140687
580	20	1.0	274695	2	AC127582	Mus muscu	653	19	1.0	586	11	G63087	G63087 SHGC-140687
581	20	1.0	278572	10	AF287263	Mus muscu	654	19	1.0	586	11	G63087	G63087 SHGC-140687
582	20	1.0	283050	1	BX294150	Mus muscu	655	19	1.0	586	11	G63087	G63087 SHGC-140687
583	20	1.0	283274	2	AC055759	White sapi	656	19	1.0	586	11	G63087	G63087 SHGC-140687
584	20	1.0	292967	14	AF369029	White sapi	657	19	1.0	586	11	G63087	G63087 SHGC-140687
585	20	1.0	294272	2	AC103344	Rattus no	658	19	1.0	586	11	G63087	G63087 SHGC-140687
586	20	1.0	295400	2	AP005039	Streptomy	659	19	1.0	586	11	G63087	G63087 SHGC-140687
587	20	1.0	299925	8	AE017051	Oryza sat	660	19	1.0	586	11	G63087	G63087 SHGC-140687
588	20	1.0	300023	8	AE017051	Oryza sat	661	19	1.0	586	11	G63087	G63087 SHGC-140687
589	20	1.0	300023	8	AE017051	Oryza sat	662	19	1.0	586	11	G63087	G63087 SHGC-140687
590	20	1.0	300029	8	AE017051	Oryza sat	663	19	1.0	586	11	G63087	G63087 SHGC-140687
591	20	1.0	300800	1	SC093911	Streptomy	664	19	1.0	586	11	G63087	G63087 SHGC-140687
592	20	1.0	300964	8	AE016890	Eremothec	665	19	1.0	586	11	G63087	G63087 SHGC-140687
593	20	1.0	303228	8	AE017070	Oryza sat	666	19	1.0	586	11	G63087	G63087 SHGC-140687
594	20	1.0	304297	8	AE017088	Oryza sat	667	19	1.0	586	11	G63087	G63087 SHGC-140687
595	20	1.0	305107	6	AX151396	Sequence	668	19	1.0	586	11	G63087	G63087 SHGC-140687
596	20	1.0	305107	14	AF332093	White sapi	669	19	1.0	586	11	G63087	G63087 SHGC-140687
597	20	1.0	305166	3	AE003601	White sapi	670	19	1.0	586	11	G63087	G63087 SHGC-140687
598	20	1.0	307287	14	AF440570	White sapi	671	19	1.0	586	11	G63087	G63087 SHGC-140687
599	20	1.0	318505	2	AC123174	Rattus no	672	19	1.0	586	11	G63087	G63087 SHGC-140687
600	20	1.0	324367	8	AE017091	Oryza sat	673	19	1.0	586	11	G63087	G63087 SHGC-140687
601	20	1.0	336363	2	AC139857	Mus muscu	674	19	1.0	586	11	G63087	G63087 SHGC-140687
602	19	1.0	189	6	AX698079	Sequence	675	19	1.0	586	11	G63087	G63087 SHGC-140687
603	19	1.0	201	11	BV201540	Sequence	676	19	1.0	586	11	G63087	G63087 SHGC-140687

677	1.0	1107	8	AF510222	Saccharom	750	19	1.0	2501	6	CQ778532	CQ778532 Sequence
678	1.0	1120	9	HSU15963	Human versi	751	19	1.0	2513	8	AK101520	AK101520 Oryza sat
679	1.0	1128	8	AY045684	Arabidops	752	19	1.0	2601	6	BD180282	BD180282 Highly th
680	1.0	1128	8	AF510223	Saccharom	753	19	1.0	2603	6	AX714069	AX714069 Sequence
C 681	1.0	1130	8	AK121889	Arabidops	C 754	19	1.0	2603	9	AK056137	AK056137 Homo sapi
682	1.0	1140	5	AF145944	Barbus lu	C 755	19	1.0	2655	10	BC031135	BC031135 Mus muscu
683	1.0	1140	5	AF145947	Barbus ca	756	19	1.0	2746	6	AX883125	AX883125 Sequence
684	1.0	1140	5	AF180831	Barbus ca	757	19	1.0	2746	6	BD160141	BD160141 Primer fo
685	1.0	1140	5	AF180852	Barbus ch	758	19	1.0	2746	8	AK023671	AK023671 Homo sapi
686	1.0	1140	5	AF180855	Barbus ha	759	19	1.0	2767	8	AY485636	AY485636 Uetilla
687	1.0	1140	5	AF180864	Barbus wu	C 760	19	1.0	2795	10	BC016131	BC016131 Oryza sat
688	1.0	1140	5	AF180866	Varicorhi	C 761	19	1.0	2795	8	AK193255	AK193255 Oryza sat
689	1.0	1140	5	AF180876	Barbus ae	762	19	1.0	3064	8	AY035076	AY035076 Arabidops
690	1.0	1140	5	AF180877	Barbus po	763	19	1.0	3073	8	AK099582	AK099582 Oryza sat
691	1.0	1141	5	AF287431	Barbus gr	764	19	1.0	3085	9	AK074251	AK074251 Homo sapi
692	1.0	1141	5	AF287448	Barbus wu	C 765	19	1.0	3104	8	AK065680	AK065680 Oryza sat
693	1.0	1141	5	AF288486	Barbus ca	C 766	19	1.0	3310	14	AB102675	AB102675 Rosellini
694	1.0	1142	5	AF201581	Campylomo	C 767	19	1.0	3517	6	AX746577	AX746577 Sequence
C 695	1.0	1173	8	AY559047	Oryza sat	C 768	19	1.0	3517	6	AK090691	AK090691 Homo sapi
696	1.0	1173	8	AF510224	Saccharom	C 769	19	1.0	3621	6	AR300472	AR300472 Sequence
697	1.0	1173	8	AF510224	Saccharom	C 770	19	1.0	3621	6	AR428749	AR428749 Sequence
698	1.0	1238	8	BC040733	Homo sapi	C 771	19	1.0	3621	6	AR442838	AR442838 Sequence
C 699	1.0	1238	8	AK065256	Oryza sat	C 772	19	1.0	3641	6	CQ716253	CQ716253 Sequence
700	1.0	1260	8	AF510225	Saccharom	C 773	19	1.0	3641	6	HIMECTPH	HIMECTPH Human prote
C 701	1.0	1281	8	AF510226	Saccharom	C 774	19	1.0	3783	6	AR300471	AR300471 Sequence
C 702	1.0	1307	8	AY088839	Arabidops	C 775	19	1.0	3783	6	AR442837	AR442837 Sequence
C 703	1.0	1336	10	XLP40PK	X53962 Xenopus MOI	C 776	19	1.0	3807	6	AR442837	AR442837 Sequence
704	1.0	1447	5	CR523638	Gallus ga	C 777	19	1.0	3807	6	CQ730760	CQ730760 Sequence
705	1.0	1467	3	AF216742	Typanoso	C 778	19	1.0	3879	6	CQ612468	CQ612468 Sequence
C 706	1.0	1528	8	NTA438265	Nicotiana	C 779	19	1.0	4010	9	AK122932	AK122932 Homo sapi
707	1.0	1531	8	BT006037	Arabidops	C 780	19	1.0	4174	6	CQ611597	CQ611597 Sequence
C 708	1.0	1536	10	AY640307	Mus muscu	C 781	19	1.0	4174	6	CQ577748	CQ577748 Sequence
C 709	1.0	1542	8	BT008878	Arabidops	C 782	19	1.0	4277	6	AX468106	AX468106 Sequence
C 710	1.0	1572	8	AY093133	Arabidops	C 783	19	1.0	4308	5	GGRNACMET	GGRNACMET X84044 G-gallus mr
711	1.0	1582	8	AK064240	Oryza sat	C 784	19	1.0	4369	5	BT010034	BT010034 Drosophi
712	1.0	1583	8	AB090881	Aster tti	C 785	19	1.0	4456	3	CQ591494	CQ591494 Sequence
713	1.0	1650	8	AK103739	Oryza sat	C 786	19	1.0	4461	6	CQ727154	CQ727154 Sequence
714	1.0	1659	9	AK128818	Homo sapi	C 787	19	1.0	4515	6	CQ574682	CQ574682 Sequence
715	1.0	1704	6	AX652967	Sequence	C 788	19	1.0	4624	9	AF227905	AF227905 Homo sapi
C 716	1.0	1716	8	AY062534	Arabidops	C 789	19	1.0	4927	9	AK129214	AK129214 Mus muscu
C 717	1.0	1718	8	BC071687	Homo sapi	C 790	19	1.0	5007	3	BT010212	BT010212 Drosophi
C 718	1.0	1731	8	AF268870	Aspergilli	C 791	19	1.0	5042	6	AX405692	AX405692 Sequence
C 719	1.0	1743	8	AF094825	Birassica	C 792	19	1.0	5042	6	AX405692	AX405692 Sequence
C 720	1.0	1750	8	AK122010	Oryza sat	C 793	19	1.0	5053	6	AX211482	AX211482 Sequence
C 721	1.0	1757	8	AY092962	Arabidops	C 794	19	1.0	5053	6	AX085613	AX085613 Sequence
C 722	1.0	1790	10	BC057448	Mus muscu	C 795	19	1.0	5053	6	AF200359	AF200359 Rattus no
C 723	1.0	1796	10	BC026588	Mus muscu	C 796	19	1.0	5242	10	BC049106	BC049106 Mus muscu
C 724	1.0	1831	3	AK069193	Oryza sat	C 797	19	1.0	5252	9	AB018345	AB018345 Homo sapi
C 725	1.0	1927	3	AY122622	Rhynchopu	C 798	19	1.0	5252	10	BC068283	BC068283 Mus muscu
726	1.0	1933	8	AK093415	Homo sapi	C 799	19	1.0	5543	10	BC068283	BC068283 Mus muscu
727	1.0	1978	8	AK117505	Arabidops	C 800	19	1.0	5580	10	BC068283	BC068283 Mus muscu
728	1.0	2000	6	AX655891	Sequence	C 801	19	1.0	5597	6	AR300462	AR300462 Sequence
729	1.0	2011	9	AK128817	Homo sapi	C 802	19	1.0	5597	6	AR428739	AR428739 Sequence
730	1.0	2013	8	BT005955	Arabidops	C 803	19	1.0	5597	6	AR442828	AR442828 Sequence
731	1.0	2025	6	AX088885	Sequence	C 804	19	1.0	6616	6	AX345377	AX345377 Sequence
732	1.0	2025	6	AX825715	Sequence	C 805	19	1.0	6625	6	CQ599108	CQ599108 Sequence
C 733	1.0	2026	5	OMY427867	Oncothyrc	C 806	19	1.0	6684	6	AX252004	AX252004 Sequence
734	1.0	2037	8	AK106734	Oryza sat	C 807	19	1.0	6754	6	AX348777	AX348777 Sequence
735	1.0	2063	9	AK074376	Homo sapi	C 808	19	1.0	6802	5	AY217453	AY217453 Oncothyrc
736	1.0	2094	9	BC044310	Homo sapi	C 809	19	1.0	6802	5	AY217453	AY217453 Oncothyrc
737	1.0	2104	6	AX088884	Sequence	C 810	19	1.0	9567	3	DMU25586	DMU25586 Drosophi
738	1.0	2104	6	AX825714	Sequence	C 811	19	1.0	9567	3	AX664484	AX664484 Sequence
C 739	1.0	2158	10	BC058764	Mus muscu	C 812	19	1.0	12257	1	AB000973	AB000973 Pyrobacti
740	1.0	2158	10	AY113877	Arabidops	C 813	19	1.0	12499	2	AC017696	AC017696 Drosophi
741	1.0	2227	5	BC067309	Xenopus t	C 814	19	1.0	12839	6	CQ584729	CQ584729 Sequence
C 742	1.0	2260	14	PEHLE671V	Human papil	C 815	19	1.0	13514	6	CQ576587	CQ576587 Sequence
743	1.0	2263	8	AK072690	Oryza sat	C 816	19	1.0	15579	6	CQ806572	CQ806572 Sequence
744	1.0	2320	8	AK118488	Arabidops	C 817	19	1.0	15579	6	CQ806572	CQ806572 Sequence
745	1.0	2381	10	BC023910	Mus muscu	C 818	19	1.0	15579	6	AX795680	AX795680 Sequence
C 746	1.0	2421	6	AR392138	Sequence	C 819	19	1.0	15579	6	AX795680	AX795680 Sequence
C 747	1.0	2421	6	BD082200	Activity	C 820	19	1.0	15579	6	AX795680	AX795680 Sequence
C 748	1.0	2487	6	AR392148	Sequence	C 821	19	1.0	15579	6	AX822129	AX822129 Sequence
C 749	1.0	2487	10	AF068198	Mus muscu	C 822	19	1.0	15579	6	AX822282	AX822282 Sequence

823	19	1.0	16579	6	AX825594	AX825594 Sequence	C 896	19	1.0	98942	8	F24U5	AC008075 Arabidops
C 824	19	1.0	16579	6	AX825601	AX825601 Sequence	897	19	1.0	98955	9	AC008886	AC008886 Homo sapi
825	19	1.0	16579	6	AX825769	AX825769 Sequence	898	19	1.0	99322	2	AC046184	AC046184 Homo sapi
C 826	19	1.0	16579	6	AX825922	AX825922 Sequence	899	19	1.0	99960	8	TBP20	AC018748 Sequence
C 827	19	1.0	16750	6	AX251068	AX251068 Sequence	C 900	19	1.0	102178	8	AP003803	AP003803 Oryza sat
C 828	19	1.0	16750	6	AX345423	AX345423 Sequence	C 901	19	1.0	104481	2	AP003844	AP003844 Oryza sat
C 829	19	1.0	18964	8	CRE242525	CRE242525 Sequence	C 902	19	1.0	104485	9	AC069439	AC069439 Homo sapi
830	19	1.0	22022	8	AB025640	AB025640 Arabidops	903	19	1.0	105787	9	AC113367	AC113367 Homo sapi
831	19	1.0	23889	3	CEB02A10	CEB02A10 Arabidops	904	19	1.0	106742	8	AP003835	AP003835 Homo sapi
832	19	1.0	25537	2	AC014683	AC014683 Drosophi	905	19	1.0	106992	9	AC092614	AC092614 Homo sapi
833	19	1.0	28078	2	CEP21F12	CEP21F12 Drosophi	C 906	19	1.0	107480	9	AL596094	AL596094 Human DNA
C 834	19	1.0	29594	2	AC014129	AC014129 Drosophi	C 907	19	1.0	107621	8	AP004157	AP004157 Oryza sat
C 835	19	1.0	30480	3	CER22B3	CER22B3 Caenorhabd	C 908	19	1.0	107815	9	AC002482	AC002482 Human BAC
C 836	19	1.0	30615	2	AC018027	AC018027 Drosophi	C 909	19	1.0	108012	9	AL713868	AL713868 Human DNA
837	19	1.0	30889	2	AC019350	AC019350 Phakopsor	C 910	19	1.0	108058	8	BX908811	BX908811 Neurospor
838	19	1.0	32572	6	AX358994	AX358994 Sequence	C 911	19	1.0	108464	2	AP000710	AP000710 Homo sapi
839	19	1.0	32621	14	AF289262	AF289262 Porcine a	C 912	19	1.0	109946	5	BX324141	BX324141 Zebrafish
840	19	1.0	33169	9	AC148924	AC148924 Pan trogl	C 913	19	1.0	109964	2	AC095760	AC095760 Rattus no
C 841	19	1.0	33520	3	CER02E1	CER02E1 Caenorhabd	C 914	19	1.0	110000	2	AC095760	AC095760 Rattus no
842	19	1.0	33782	3	CEZK909	CEZK909 Caenorhabd	C 915	19	1.0	110000	2	AC096395	AC096395 Rattus no
843	19	1.0	34934	3	AC148914	AC148914 Pan trogl	C 916	19	1.0	110000	2	AC103465	AC103465 Rattus no
844	19	1.0	35955	3	CEP53B7	CEP53B7 Caenorhabd	C 917	19	1.0	110000	2	AC110828	AC110828 Rattus no
C 845	19	1.0	37497	2	AC0017356	AC0017356 Drosophi	C 918	19	1.0	110000	2	AC110829	AC110829 Rattus no
C 846	19	1.0	39366	9	BS000569	BS000569 Pan trogl	C 919	19	1.0	110000	2	AC110950	AC110950 Rattus no
C 847	19	1.0	39534	3	CEZK643	CEZK643 Caenorhabd	C 920	19	1.0	110000	2	AC113742	AC113742 Rattus no
C 848	19	1.0	43570	8	AB019231	AB019231 Arabidops	C 921	19	1.0	110000	2	AC115429	AC115429 Rattus no
C 849	19	1.0	43802	3	CEK07F5	CEK07F5 Caenorhabd	C 922	19	1.0	110000	2	AC115429	AC115429 Rattus no
850	19	1.0	44057	9	HSCN37F10	HSCN37F10 Human DNA	C 923	19	1.0	110000	2	AC115429	AC115429 Rattus no
851	19	1.0	50840	9	AP002492	AP002492 Homo sapi	C 924	19	1.0	110000	2	AC128812	AC128812 Rattus no
C 852	19	1.0	52000	9	AP002492	AP002492 Homo sapi	C 925	19	1.0	110000	2	AC131059	AC131059 Rattus no
C 853	19	1.0	53025	9	AC118458	AC118458 Homo sapi	C 926	19	1.0	110000	2	AC149068	AC149068 Rattus no
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C 857	19	1.0	57281	2	AC104861	AC104861 Mus muscu	C 930	19	1.0	110000	8	CR380959	CR380959 Rattus no
C 858	19	1.0	57652	2	AC104861	AC104861 Mus muscu	C 931	19	1.0	110000	8	CR382129	CR382129 Rattus no
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C 860	19	1.0	60461	2	AC008063	AC008063 Homo sapi	C 933	19	1.0	110000	8	ATAC016839	ATAC016839 Homo sapi
C 861	19	1.0	62458	2	AC067878	AC067878 Homo sapi	C 934	19	1.0	111122	8	AC145367	AC145367 Oryza sat
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C 872	19	1.0	72450	2	AC025914	AC025914 Mus muscu	C 945	19	1.0	114817	8	AC149836	AC149836 Zea mays
C 873	19	1.0	74997	10	AL732362	AL732362 Mouse DNA	C 946	19	1.0	116803	9	AC0131904	AC0131904 Homo sapi
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C 881	19	1.0	85303	2	AC126918	AC126918 Gallus ga	C 954	19	1.0	122464	8	AP003858	AP003858 Oryza sat
C 882	19	1.0	85567	8	AB016878	AB016878 Arabidops	C 955	19	1.0	122571	9	AF064859	AF064859 Homo sapi
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C 886	19	1.0	87538	2	AL158200	AL158200 Human DNA	C 959	19	1.0	125151	9	AC0121340	AC0121340 Homo sapi
C 887	19	1.0	88639	2	AC106831	AC106831 Homo sapi	C 960	19	1.0	125285	9	ATF4420	ATF4420 Homo sapi
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C 890	19	1.0	92620	8	AB026636	AB026636 Arabidops	C 963	19	1.0	125787	9	HSJ13817A	HSJ13817A Homo sapi
C 891	19	1.0	93951	8	AC010483	AC010483 Homo sapi	C 964	19	1.0	125787	9	HSJ13817A	HSJ13817A Homo sapi
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893	19	1.0	95932	8	AB017060	AB017060 Oryza sat	C 966	19	1.0	126332	8	AC137621	AC137621 Oryza sat
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Dp	1201	AAGCGTTCAACATATGATGATTTCAAGTTTGAAGTTAAGTTGAGTTGGTCTTGGTCTT	12600
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RESULT 4
LOCUS      AY028699                      2189 bp    mRNA    linear    PLN 26-MAR-2001
DEFINITION Brassica napus receptor protein kinase PERK1 mRNA, complete cds.
ACCESSION  AY028699
VERSION     AY028699.1  GI:13447448
KEYWORDS
SOURCE      Brassica napus (rape)
ORGANISM    Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 2189)
AUTHORS     Silva,N.F. and Goring,D.R.
TITLE       Characterization of a novel Brassica napus receptor protein kinase
            PERK1
JOURNAL     Unpublished
            2 (bases 1 to 2189)
            Silva,N.F. and Goring,D.R.
            Direct Submission
            Submitted (19-MAR-2001) Biology, York University, 4700 Keele
            Street, Toronto, Ontario M3J 1P3, Canada
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Db 2017 GGTATAGTGAACCTTCTCTTTAA 2040

RESULT 5
AY536856 668 bp mRNA linear PLN 20-MAR-2004

LOCUS Arabidopsis thaliana putative protein kinase (At3g24550) mRNA.

DEFINITION partial cds.

ACCESSION AY536856

VERSION AY536856.1 GI:45454229

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 668)
Kurtz, J. and Leister, D.
Protein kinases in chloroplasts
Unpublished
2 (bases 1 to 668)
Kurtz, J. and Leister, D.
Direct Submission
Submitted (22-JAN-2004) Leister Laboratory, Max Planck Institut
fuern Zuechtungsforchung, Carl-von-Linne Weg 10, Cologne 50829,
Germany

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5e-24;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 AACATGCTCTATGATGACGAGCTTAGTGACTGGGACGACCATGCTTAACGAGCA 1491

Db 178 AACATGCTCTATGATGACGAGCTTAGTGACTGGGACGACCATGCTTAACGAGCA 237

QY 1492 TCTGAG 1497

Db 238 TCTGAG 243

RESULT 6
AX825738 1959 bp DNA linear PAT 11-DEC-2003

LOCUS Arabidopsis thaliana putative protein kinase (At3g24550) mRNA.

DEFINITION Sequence 36 from Patent WO03072763.

ACCESSION AX825738

VERSION AX825738.1 GI:39751255

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
Goring, D., Silva, N. and Haffani, Y. Z.
Increasing plant seed production
Patent: WO 03072763-A 36 04-SEP-2003;
Goring, Daphne (CA); Silva, Nancy (CA); Haffani, Yoser, Z. (CA)

FEATURES
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ORIGIN
Query Match 3.4%; Score 66; DB 6; Length 1959;
Best Local Similarity 100.0%; Pred. No. 4.7e-24;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1447 AACATGCTCTATGATGACGAGCTTAGTGACTGGGACGACCATGCTTAACGAGCA 1506

QY 1492 TCTGAG 1497

Db 1507 TCTGAG 1512

RESULT 7
BT008400 1959 bp mRNA linear PLN 15-MAY-2003

LOCUS Arabidopsis thaliana At3g24550 gene, complete cds.

DEFINITION BT008400

ACCESSION BT008400.1 GI:30725473

VERSION BT008400.1

KEYWORDS FLI CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1959)
Cheuk, R., Chen, H., Kim, C.J., Shin, P., Bowser, L., Carninci, P.,
Dale, J.M., Hayashizaki, Y., Hsuan, Y.W., Ishida, J., Jones, T.,
Kamuya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,
Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W.,
Theologis, A. and Ecker, J.R.
Arabidopsis ORF clones

TITLE Arabidopsis ORF clones

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1959)
Cheuk, R., Chen, H., Kim, C.J., Shin, P., Bowser, L., Carninci, P.,
Dale, J.M., Hayashizaki, Y., Hsuan, Y.W., Ishida, J., Jones, T.,
Kamuya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,
Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W.,
Theologis, A. and Ecker, J.R.
Direct Submission

JOURNAL Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
(SIGAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

COMMENT
The discrepancy does not affect the protein sequence.
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamuya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.


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LCKKRRRRHDEALVYVPPPPSPGKAGGPGGQOOQMOONASIGVAILVTLICL
PKPSPPPRPPKPPPPPPAPFMSGSGSDSLDVLVPPSPGLVGSKSTPYEEISRA
TNGSEANLLGGGFGYVHGKILPBGKGVAAVYVGGGSGGGRERQAEVILLRHHYR
HLVSLIGCYMAGVORLLVYEPYNNLLFEHLHGKRPRMENSSTRKILAGSAGLSYL
HEDNPKLIHRHDIKASNLILDPKFAKADPAVDLADTHTHTSTGVTGGTAYLPE
YAASKLTEKSDVFSFGVLLLELTGRRPVDANNVYVDSLVDMARPLINNASEGDPE

```

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAP1 cDNAs: Cheuk, R., Chen, H., Kim, C. J., Kosemema, E., Meyers, M. C., Shim, P., Banh, J., Bowser, L., Dale, J. M., Goldsmith, A. D., Jiang, P. X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Liu, S. X., Miranda, M., Nguyen, M., Onders, C. S., Palm, C. J., Pham, P. K., Quach, H. L., Southwick, A., Tang, C. C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R. W., Theologis, A., and Ecker, J. R.

1432 AACATGTTCTATGTAGATGACAGCTTAGTTGACTGGGACGACCATTGTCTAACGAGCA 1491

Db 1553 AACATGTCATGATGATACAGCTTAGTGAAGTGGCGACGACCATGCTTACGAGCA 1612

QY 1492 TCTGAG 1497

Db 1613 TCTGAG 1618

RESULT 14

AB020746 79706 bp DNA linear PLN 14-FEB-2004

LOCUS Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24.

DEFINITION AB020746 BA000014

ACCESSION AB020746.1 GI:39859949

VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PubMed 10907853

2 (bases 1 to 79706)

Kaneko,T., Kato,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.

Structural analysis of Arabidopsis thaliana chromosome 3. II.

Sequence features of the 4,251,695 bp regions covered by 90 P1, PAC

and BAC clones

DNA Res. 7 (3), 217-221 (2000)

20363099

10907853

2 (bases 1 to 79706)

Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.

Direct Submission

Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research

Institute, Department of Plant Gene Research, 1532-3, Yana,

Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,

Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see

http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MOB24

Genes with similarity to proteins in the databases are described in

'product' or 'note' qualifiers. Genes that have no significant

protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Graal

(Informatics Group, Oak Ridge National Laboratory,

http://combio.ornl.gov/Graal-1.3/),

GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),

NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of

Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and

SplicePredictor (Volker Brendel, Stanford University,

http://gremlii.zool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE

(Sean Eddy, Washington University School of Medicine, St. Louis,

http://genome.wustl.edu/eddy/tRNAscan-SE/).

This sequence may not be the entire insert of this clone. It may be

shorter because we remove overlaps between neighboring submissions.

The 5' clone is MXP5 and the 3' clone is MSD24.

Location/Qualifiers

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/db_xref="taxon:3702"

/chromosome="3"

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GLSSKWSFENKLDMLCVSPKSDIGLACGVDSGEFVFNPTKVYIDKNSGPEBMDSP

GDSEEDDEDDVEYERKKVNDASVYKMLASVSEFPAKASGASGLFSNIMKFL

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REVEDIGQGVDPETPGMRPRASRLKRLDEMTFKEDKVDLSNKRKLKLOPV

CGEKKVNEGTQFEMLESRIIDANRRRPDDLYPRKTHIHDPVFKMSAKOXYMS

VSEYMDIVLFKRVGFYELVLELDELKHELDKMTMGSGVCKRGVIGISGSDIVAV

OKLARGVGRIBQLTSDQAKARGANTITPRKLVQVLPSTASGNIGPDVHLLA

IKELMELOKRSYVGVFAVDCALRFWVGSISDASCALGALLMQVSEPEVLYDSK

GLSREOKALRYKTLTGSTAVQALAPVQVAGDIDAGVNNIESNGYFKGSSBWNCA

VGINLNCVYALSAIGELINHLISRLKLEVDLKHGDIIPYVGRGLRIDQTMNLIF

NNSCDGPGSTLYKYINDCVSPGKRLINMTCHPLKDYESIKKRLADVEEPTANSBS

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GKSKTLIRATCLAVIFPAQIGCVYVCSCEISVDITFYRLGASDRIMTGSTNLEET

ERASVIONATQDSVILFDELGRGTPDGVATVAVSFRRHVEVQCRMLPATYHPLT

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NIIVFGSTAGALASHMDVDKVSFTSTVGAKIMQAAASNLKRLVLEJGGSPLI

IFNDADIDKADAILLGCFFYKKEIICVASSVFPQEBGYDVAASNLKRLVLEKADWVGP

FDSTAROGPOVDKROPEKILSYIEHKNKGELTLTGKALIDKCYFIQPTIFAVTED

MKYQDERFGVYSLMKFKTYEIGIKCANNTKYGALAGIISODIDILINTVRSIKAGI

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CDS

CDS
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EKYAKVADGCTSLQIKNHGDEKSGNSYKLLIVSSLSIAHTVREYKAGDEO
EDNGKRAVAVGEGNSFGNDGIRSRKSLALPSQOKKDLGEEELTPRGVAAAC
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TNHNELVITWIKNSLRPLVSSRTFTGICLKNNGIMPETSPRACDCHPSATI
CISPHLIGISFKQSCISRSVKAHSIRISKEVNPFLITTESSPHALVVGKIGIMI
TSPSGDYORFNNLSHSPYLITFEKORFNIIKSIHDLQSGKNGMISSPMDYR
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LI"
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1579 GCTGGCGCTGTGTGCTGCCATTGAGCTGCCGAGACCTCGCATGAGCCAG 1629
Db 54008 GCTGGCGCTGTGTGCTGCCATTGAGCTGCCGAGACCTCGCATGAGCCAG 54058

RESULT 15
AY0899024
LOCUS
DEFINITION
Arabidopsis thaliana clone 17909 mRNA, complete sequence.
ACCESSION
AY0899024
VERSION
AY0899024.1
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana (thale cress)
Bukarjaya; Vitridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2324)
Haas,B.U., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
22088475
MEDLINE
12093376
PUBMED
2 (bases 1 to 2324)
REFERENCE
Broyer,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 2324)
Broyer,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or later ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
location/Qualifiers
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/organism="Arabidopsis thaliana"
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ORIGIN

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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1585 GCTTGTGTCGCGCATTCAGCTCGCGGAGACCTCGCATGAGCCAGAT 1631
Db 1700 GCTTGTGTCGCGCATTCAGCTCGCGGAGACCTCGCATGAGCCAGAT 1746

Search completed: November 13, 2004, 14:21:32
Job time : 5615 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 10:56:30 ; Search time 651 Seconds

(without alignments)
15675.690 Million cell updates/sec

Title: US-10-069-304-1

Perfect score: 1944

Sequence: 1 atgtcctcgggcgcgtctcc.....atagtggaacctctttaa 1944

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1944	100.0	1944	4	Aaf77094 Brassica
2	1944	100.0	1944	10	AcF36548 B. napus
3	1944	100.0	2189	10	AcF36548 B. napus
4	66	3.4	1959	10	AcF36557 A. thaliana
5	47	2.4	2324	3	AAK36968 Arabidops
6	27	1.4	685	10	ADK53814 Plant DNA
7	26	1.3	1515	9	ACF36555 Z. mays P
8	26	1.3	110000	3	AAAF22305_06 Continuation (7 of
9	26	1.3	110000	3	AAAF22305_07 Continuation (8 of
10	24	1.2	1389	8	ADA70853 Rice gene
11	24	1.2	1515	9	ADA70853 Rice gene
12	24	1.2	1515	9	ADA70853 Rice gene
13	24	1.2	1515	9	ADA70853 Rice gene
14	24	1.2	1515	9	ADA70853 Rice gene
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Aas84463 DNA encod
AdB61530 Hepatocyt
AdB61585 Hepatocyt
Abv99385 Human NOV
Aad48130 Human C-M
AdA30158 Human hep
AdC78858 Human PRO
AdF09640 Human hep
Aad47594 Human hep
AdJ74837 Marker ge
AdI61128 Human pro
AdB30165 Hepatocyt
Aav20444 Human c-m
AdI42797 Human TPR
AdI57191 Human GME
AdM33390 Human PRO
Continuation (39 o
Continuation (10 o
AdA30166 Hepatocyt
Aad30797 Hansenula
Aad47060 ZMPK1 hom
Aad44708 Novel pro
AdI29406 Human MAR
AdI18074 Human sof
Abn59741 Novel hum
Aaf77095 Arabidops
AcF36550 Arabidops
Aad7043 Human DNA
Aaf22304 Arabidops
Aaf22300 BAC conta
AdC87622 Human GPC
AdC87621 Human GPC
AbI86637 Human ova
AdF58261 Human pol
AbK62007 Arabidops
Aaf97928 Human sec
AdB95095 A. thaliana
AdM45539 Insect re
AdI42029 Plant tra
AdO02580 Soybean o
AdI42031 Plant tra
AdO02582 Soybean o
Aac49631 Arabidops
AdO2670 Pseudomon
AdO2777 Pseudomon
AdO57240 DNA encod
Aad4411 Human hun
AdO2683 Pseudomon
AdA72522 Rice gene
Aad44410 Human hun
Aac49896 Arabidops
Aaf84403 Human MAV
AdC23249 Seed deve
AdI45233 Human ova
AdF65510 Potarto re
AdF65508 Potarto re
AdF65509 Potarto re
AdF65511 Potarto re
Aaf77096 Arabidops
AcF36551 Arabidops
AbI17801 Aspergill
AbI19615 Aspergill
AbI99364 Mouse isc
AaI43970 Exotic ge
Aad62995 Human CDN
Aaf9273 Eucalyptu
Aaf62819 Shrimp wh
AaI36240 Human mus
Abx59228 CDNA enco
AdJ29978 Human mus
AaI36242 Human mus
AdX59230 CDNA enco
AdJ29980 Human mus

C 95	1.0	5720	4	AAFP97891	Aaf97891 Human sec	C 168	1.0	2421	2	AAV49808	Aav49808 Mouse ADN
C 96	1.0	5769	4	ABA06468	Abao6468 Human cdn	C 169	1.0	2421	3	AAAD00747	Aad00747 Mouse Act
C 97	1.0	5769	4	ABV83805	Abv83805 Human pol	C 170	1.0	2430	3	AAH27430	Aah27430 Human UDP
C 98	1.0	5868	3	AAA28019	Aaa28019 Quelling	C 171	1.0	2487	3	AAAD00748	Aad00748 Mouse Act
C 99	1.0	6916	3	AAA28019	Aaa28019 Quelling	C 172	1.0	2487	3	AAAD00748	Aad00748 Mouse Act
C 100	1.0	7142	6	ABSS8372	Abss8372 Protein m	C 173	1.0	2746	4	AAH18149	Aah18149 Human cod
C 101	1.0	8029	3	AAI62036	Aai62036 Human cel	C 174	1.0	2820	4	AAH18149	Aah18149 Human cod
C 102	1.0	41100	4	AAI10873	Aai10873 Human gen	C 175	1.0	2820	4	AAH18149	Aah18149 Human cod
C 103	1.0	97700	10	ADLI3678	Adli3678 Osteoarct	C 176	1.0	3517	10	ADBE1948	Adbe1948 Human cdn
C 104	1.0	305107	4	AAH62689	Aah62689 Strimp wh	C 177	1.0	3517	10	ADBE1948	Adbe1948 Human cdn
C 105	1.0	105	12	ACH81173	Ach81173 Human gen	C 178	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 106	1.0	141	12	ACH82031	Ach82031 Human gen	C 179	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 107	1.0	189	8	ACH84440	Ach84440 Clone T11	C 180	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 108	1.0	189	8	ACH84440	Ach84440 Clone T11	C 181	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 109	1.0	268	12	ADP55597	Adp55597 Cotion ex	C 182	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 110	1.0	268	12	ADP55597	Adp55597 Cotion ex	C 183	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 111	1.0	323	5	AAK8282	Aak8282 Human dig	C 184	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 112	1.0	323	5	AAK8282	Aak8282 Human dig	C 185	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 113	1.0	323	5	AAK8282	Aak8282 Human dig	C 186	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 114	1.0	333	2	AAI1309	Aai1309 Allergen	C 187	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 115	1.0	358	2	AAV83357	Aav83357 Breast ca	C 188	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 116	1.0	358	2	AAV83357	Aav83357 Breast ca	C 189	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 117	1.0	358	2	AAV83357	Aav83357 Breast ca	C 190	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 118	1.0	358	2	AAV83357	Aav83357 Breast ca	C 191	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 119	1.0	358	2	AAV83357	Aav83357 Breast ca	C 192	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 120	1.0	358	2	AAV83357	Aav83357 Breast ca	C 193	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 121	1.0	358	2	AAV83357	Aav83357 Breast ca	C 194	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 122	1.0	423	8	ABX42341	Abx42341 Bovine ES	C 195	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 123	1.0	423	8	ABX42341	Abx42341 Bovine ES	C 196	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 124	1.0	463	3	AAI15613	Aai15613 Probe #55	C 197	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 125	1.0	463	3	AAI15613	Aai15613 Probe #55	C 198	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 126	1.0	463	3	AAI15613	Aai15613 Probe #55	C 199	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 127	1.0	463	3	AAI15613	Aai15613 Probe #55	C 200	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 128	1.0	463	3	AAI15613	Aai15613 Probe #55	C 201	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 129	1.0	463	3	AAI15613	Aai15613 Probe #55	C 202	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 130	1.0	463	3	AAI15613	Aai15613 Probe #55	C 203	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 131	1.0	463	3	AAI15613	Aai15613 Probe #55	C 204	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 132	1.0	463	3	AAI15613	Aai15613 Probe #55	C 205	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 133	1.0	463	3	AAI15613	Aai15613 Probe #55	C 206	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 134	1.0	463	3	AAI15613	Aai15613 Probe #55	C 207	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 135	1.0	463	3	AAI15613	Aai15613 Probe #55	C 208	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 136	1.0	463	3	AAI15613	Aai15613 Probe #55	C 209	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 137	1.0	463	3	AAI15613	Aai15613 Probe #55	C 210	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 138	1.0	463	3	AAI15613	Aai15613 Probe #55	C 211	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 139	1.0	463	3	AAI15613	Aai15613 Probe #55	C 212	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 140	1.0	463	3	AAI15613	Aai15613 Probe #55	C 213	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 141	1.0	463	3	AAI15613	Aai15613 Probe #55	C 214	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 142	1.0	463	3	AAI15613	Aai15613 Probe #55	C 215	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 143	1.0	463	3	AAI15613	Aai15613 Probe #55	C 216	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 144	1.0	463	3	AAI15613	Aai15613 Probe #55	C 217	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 145	1.0	463	3	AAI15613	Aai15613 Probe #55	C 218	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 146	1.0	463	3	AAI15613	Aai15613 Probe #55	C 219	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 147	1.0	463	3	AAI15613	Aai15613 Probe #55	C 220	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 148	1.0	463	3	AAI15613	Aai15613 Probe #55	C 221	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 149	1.0	463	3	AAI15613	Aai15613 Probe #55	C 222	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 150	1.0	463	3	AAI15613	Aai15613 Probe #55	C 223	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 151	1.0	463	3	AAI15613	Aai15613 Probe #55	C 224	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 152	1.0	463	3	AAI15613	Aai15613 Probe #55	C 225	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 153	1.0	463	3	AAI15613	Aai15613 Probe #55	C 226	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 154	1.0	463	3	AAI15613	Aai15613 Probe #55	C 227	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 155	1.0	463	3	AAI15613	Aai15613 Probe #55	C 228	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 156	1.0	463	3	AAI15613	Aai15613 Probe #55	C 229	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 157	1.0	463	3	AAI15613	Aai15613 Probe #55	C 230	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 158	1.0	463	3	AAI15613	Aai15613 Probe #55	C 231	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 159	1.0	463	3	AAI15613	Aai15613 Probe #55	C 232	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 160	1.0	463	3	AAI15613	Aai15613 Probe #55	C 233	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 161	1.0	463	3	AAI15613	Aai15613 Probe #55	C 234	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 162	1.0	463	3	AAI15613	Aai15613 Probe #55	C 235	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 163	1.0	463	3	AAI15613	Aai15613 Probe #55	C 236	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 164	1.0	463	3	AAI15613	Aai15613 Probe #55	C 237	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 165	1.0	463	3	AAI15613	Aai15613 Probe #55	C 238	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 166	1.0	463	3	AAI15613	Aai15613 Probe #55	C 239	1.0	3600	10	ADBE1948	Adbe1948 Human cdn
C 167	1.0	463	3	AAI15613	Aai15613 Probe #55	C 240	1.0	3600	10	ADBE1948	Adbe1948 Human cdn

C 241	18	0.9	216	4	AA148155	AA148155	Probe #16	C 314	18	0.9	375	4	ABS38806	ABS38806	Human liv
C 242	18	0.9	216	4	ABA50021	ABA50021	Human bre	C 315	18	0.9	375	5	AA105738	AA105738	Probe #57
C 243	18	0.9	216	4	ABA34989	ABA34989	Probe #13	C 316	18	0.9	375	5	ABS13305	ABS13305	Human gen
C 244	18	0.9	216	4	AAK42089	AAK42089	Human bon	C 317	18	0.9	378	12	ADP92453	ADP92453	Cotton ex
C 245	18	0.9	216	4	AAK16339	AAK16339	Human bra	C 318	18	0.9	382	4	AAK36951	AAK36951	Novel hum
C 246	18	0.9	216	4	ABA41695	ABA41695	Human liv	C 319	18	0.9	386	12	ADP94904	ADP94904	Cotton ex
C 247	18	0.9	216	5	AA108524	AA108524	Probe #85	C 320	18	0.9	393	5	AAK30684	AAK30684	DNA encod
C 248	18	0.9	216	6	ABS16131	ABS16131	Human gen	C 321	18	0.9	439	6	ABR07111	ABR07111	DNA clone
C 249	18	0.9	227	4	AA122239	AA122239	Probe #12	C 322	18	0.9	439	6	ABR07111	ABR07111	Human ova
C 250	18	0.9	227	4	ABA67317	ABA67317	Human foe	C 323	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 251	18	0.9	227	4	AA147532	AA147532	Probe #16	C 324	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 252	18	0.9	227	4	ABA49406	ABA49406	Human bre	C 325	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 253	18	0.9	227	4	ABA34408	ABA34408	Probe #12	C 326	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 254	18	0.9	227	4	AAK41441	AAK41441	Human bon	C 327	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 255	18	0.9	227	4	AAK15752	AAK15752	Human bra	C 328	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 256	18	0.9	227	4	ABA41080	ABA41080	Human liv	C 329	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 257	18	0.9	227	5	AA107937	AA107937	Probe #79	C 330	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 258	18	0.9	227	5	ABS15496	ABS15496	Human gen	C 331	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 259	18	0.9	229	2	AAV90205	AAV90205	EST clone	C 332	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 260	18	0.9	262	6	ABA85880	ABA85880	Human ova	C 333	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 261	18	0.9	265	5	ABA58299	ABA58299	Human ova	C 334	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 262	18	0.9	265	5	ABA58299	ABA58299	Human ova	C 335	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 263	18	0.9	270	6	ABL85716	ABL85716	Human pro	C 336	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 264	18	0.9	272	12	ADJ67287	ADJ67287	Human ova	C 337	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 265	18	0.9	274	10	ABA83800	ABA83800	Human ova	C 338	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 266	18	0.9	278	6	ABK79189	ABK79189	Bacillus	C 339	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 267	18	0.9	284	6	ABL72234	ABL72234	Corn taas	C 340	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 268	18	0.9	287	3	AAA43447	AAA43447	Mouse sec	C 341	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 269	18	0.9	288	12	ADJ67288	ADJ67288	Human ova	C 342	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 270	18	0.9	293	10	ABA87930	ABA87930	Corn ear-	C 343	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 271	18	0.9	297	6	ABL74547	ABL74547	Corn taas	C 344	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 272	18	0.9	300	6	ABL72346	ABL72346	Corn taas	C 345	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 273	18	0.9	300	10	ABA86248	ABA86248	Corn ear-	C 346	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 274	18	0.9	303	5	AAAD19497	AAAD19497	Corn ear-	C 347	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 275	18	0.9	306	5	AAAD19497	AAAD19497	Corn ear-	C 348	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 276	18	0.9	306	10	ABA85619	ABA85619	Corn ear-	C 349	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 277	18	0.9	308	10	ABA85640	ABA85640	Corn ear-	C 350	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 278	18	0.9	313	5	AAV14434	AAV14434	Human pro	C 351	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 279	18	0.9	321	3	ADJ57032	ADJ57032	Human pro	C 352	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 280	18	0.9	331	5	AAV23323	AAV23323	Human pro	C 353	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 281	18	0.9	331	5	AAV229173	AAV229173	Human pro	C 354	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 282	18	0.9	340	6	AAV29348	AAV29348	Calcium i	C 355	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 283	18	0.9	340	6	AAV29348	AAV29348	Calcium i	C 356	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 284	18	0.9	347	3	AAH30839	AAH30839	Human ova	C 357	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 285	18	0.9	350	3	AAH30940	AAH30940	Human col	C 358	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 286	18	0.9	355	3	AAH30940	AAH30940	Human col	C 359	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 287	18	0.9	357	6	ABN78952	ABN78952	Human pro	C 360	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 288	18	0.9	357	6	ABN78952	ABN78952	Human pro	C 361	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 289	18	0.9	360	4	ABA69977	ABA69977	Human ORF	C 362	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 290	18	0.9	360	4	ABA71815	ABA71815	Human foe	C 363	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 291	18	0.9	360	4	AAI50089	AAI50089	Human foe	C 364	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 292	18	0.9	360	4	AAI52158	AAI52158	Probe #18	C 365	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 293	18	0.9	360	4	AAK46257	AAK46257	Human bon	C 366	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 294	18	0.9	360	4	AAK44079	AAK44079	Human bon	C 367	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 295	18	0.9	360	4	AAK18186	AAK18186	Human bra	C 368	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 296	18	0.9	360	4	ABS45979	ABS45979	Human liv	C 369	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 297	18	0.9	360	4	ABS43734	ABS43734	Human gen	C 370	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 298	18	0.9	360	6	ABS20571	ABS20571	Human gen	C 371	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 299	18	0.9	361	4	AAK35824	AAK35824	Human gen	C 372	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 300	18	0.9	361	4	AAK35824	AAK35824	Human gen	C 373	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 301	18	0.9	361	4	AAK35824	AAK35824	Human gen	C 374	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 302	18	0.9	361	10	ADRA6518	ADRA6518	Human car	C 375	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 303	18	0.9	361	10	ADRA6520	ADRA6520	Human car	C 376	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 304	18	0.9	362	4	AAK35825	AAK35825	Human car	C 377	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 305	18	0.9	362	10	ADRA6519	ADRA6519	Human car	C 378	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 306	18	0.9	362	12	ADP92107	ADP92107	Cotton ex	C 379	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 307	18	0.9	375	4	AAI20031	AAI20031	Probe #99	C 380	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 308	18	0.9	375	4	ABA65059	ABA65059	Human foe	C 381	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 309	18	0.9	375	4	ABA45229	ABA45229	Probe #13	C 382	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 310	18	0.9	375	4	ABA47175	ABA47175	Human bre	C 383	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 311	18	0.9	375	4	ABA32165	ABA32165	Probe #10	C 384	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 312	18	0.9	375	4	AAK39221	AAK39221	Human bon	C 385	18	0.9	447	5	AAK57531	AAK57531	Human ova
C 313	18	0.9	375	4	AAK13482	AAK13482	Human bra	C 386	18	0.9	447	5	AAK57531	AAK57531	Human ova

C 387	18	0.9	477	4	AAK00707	AAK00707 Human bra	C 460	18	0.9	541	3	AAK69779	AAK69779 Human bra
C 388	18	0.9	477	4	ABE31956	ABE31956 Human l1v	C 461	18	0.9	542	6	ABQ45536	ABQ45536 Oligonuc1
C 389	18	0.9	477	4	ABE25748	ABE25748 Human l1v	C 462	18	0.9	542	6	ABQ45537	ABQ45537 Oligonuc1
C 390	18	0.9	477	5	AA100714	AA100714 Probe #70	C 463	18	0.9	550	6	AB199315	AB199315 Mouse isc
C 391	18	0.9	477	6	ABE00744	ABE00744 Human gen	C 464	18	0.9	564	4	AB121817	AB121817 Drosoph1l
C 392	18	0.9	477	6	ABE00927	ABE00927 Human gen	C 465	18	0.9	564	12	ACH73400	ACH73400 Human gen
C 393	18	0.9	479	4	AA113632	AA113632 Probe #35	C 466	18	0.9	569	4	AAK93276	AAK93276 Human cdn
C 394	18	0.9	479	4	ABE55343	ABE55343 Human foe	C 467	18	0.9	569	4	AAK93997	AAK93997 Human cdn
C 395	18	0.9	479	4	AA134992	AA134992 Probe #36	C 468	18	0.9	569	9	ACLI6718	ACLI6718 DNA clone
C 396	18	0.9	479	4	ABE44880	ABE44880 Human bre	C 469	18	0.9	569	12	ADL28703	ADL28703 5' end of
C 397	18	0.9	479	4	ABE25073	ABE25073 Probe #35	C 470	18	0.9	574	12	ADL30424	ADL30424 5' end of
C 398	18	0.9	479	4	AAK29044	AAK29044 Human bon	C 471	18	0.9	574	9	ACLI6723	ACLI6723 DNA clone
C 399	18	0.9	479	4	AAK03584	AAK03584 Human bra	C 472	18	0.9	578	4	AA112190	AA112190 Human bra
C 400	18	0.9	479	4	ABE28659	ABE28659 Human l1v	C 473	18	0.9	579	3	AAK77332	AAK77332 Human ORF
C 401	18	0.9	479	5	AA103516	AA103516 Probe #35	C 474	18	0.9	584	3	ACLI6722	ACLI6722 DNA clone
C 402	18	0.9	479	6	ABE03589	ABE03589 Human gen	C 475	18	0.9	586	12	ACH67835	ACH67835 Human gen
C 403	18	0.9	482	9	ACLI6725	ACLI6725 DNA clone	C 476	18	0.9	587	9	ACLI6728	ACLI6728 DNA clone
C 404	18	0.9	486	4	AA116341	AA116341 Probe #62	C 477	18	0.9	598	12	ACH70271	ACH70271 Human gen
C 405	18	0.9	486	4	ABE59169	ABE59169 Human foe	C 478	18	0.9	623	9	ACLI6727	ACLI6727 DNA clone
C 406	18	0.9	486	4	AA138923	AA138923 Probe #76	C 479	18	0.9	631	9	ACLI6723	ACLI6723 DNA clone
C 407	18	0.9	486	4	ABE27939	ABE27939 Probe #64	C 480	18	0.9	633	9	ACLI6738	ACLI6738 DNA clone
C 408	18	0.9	486	4	AAK33127	AAK33127 Human bon	C 481	18	0.9	633	9	ACLI6729	ACLI6729 DNA clone
C 409	18	0.9	486	4	AAK07360	AAK07360 Human bra	C 482	18	0.9	639	9	ACLI6735	ACLI6735 DNA clone
C 410	18	0.9	486	4	ABE32865	ABE32865 Human l1v	C 483	18	0.9	643	3	AAK33333	AAK33333 Arabidops
C 411	18	0.9	486	6	ABE07945	ABE07945 Human gen	C 484	18	0.9	647	9	ACLI6731	ACLI6731 DNA clone
C 412	18	0.9	486	10	ADL16727	ADL16727 DNA (Seq1	C 485	18	0.9	649	9	ACLI6732	ACLI6732 DNA clone
C 413	18	0.9	486	10	ADK58883	ADK58883 Plant DNA	C 486	18	0.9	652	12	ADL12937	ADL12937 Human ste
C 414	18	0.9	489	2	AAQ34771	AAQ34771 pcENP-B-1	C 487	18	0.9	674	3	AAK14190	AAK14190 Aspergill
C 415	18	0.9	494	4	AA113001	AA113001 Probe #29	C 488	18	0.9	674	12	ADK77096	ADK77096 Human cdn
C 416	18	0.9	494	4	ABE54701	ABE54701 Human foe	C 489	18	0.9	682	9	ACLI6716	ACLI6716 DNA clone
C 417	18	0.9	494	4	AA134356	AA134356 Probe #30	C 490	18	0.9	684	2	ADK01980	ADK01980 A. gossyp
C 418	18	0.9	494	4	ABE44252	ABE44252 Human bra	C 491	18	0.9	697	9	ACLI6717	ACLI6717 DNA clone
C 419	18	0.9	494	4	ABE24481	ABE24481 Probe #29	C 492	18	0.9	700	9	ACLI6721	ACLI6721 DNA clone
C 420	18	0.9	494	4	AAK28433	AAK28433 Human bon	C 493	18	0.9	702	9	ACLI6726	ACLI6726 DNA clone
C 421	18	0.9	494	4	AAK02986	AAK02986 Human bra	C 494	18	0.9	718	6	ABE77252	ABE77252 Pirog embr
C 422	18	0.9	494	4	ABE28028	ABE28028 Human l1v	C 495	18	0.9	746	6	ABE77252	ABE77252 Pirog embr
C 423	18	0.9	494	5	AA102918	AA102918 Probe #29	C 496	18	0.9	798	11	ADU11793	ADU11793 Rice CDNA
C 424	18	0.9	494	6	ABE02941	ABE02941 Human gen	C 497	18	0.9	801	11	ADU11439	ADU11439 Rice CDNA
C 425	18	0.9	496	4	ABE57350	ABE57350 Human foe	C 498	18	0.9	819	5	AAE68928	AAE68928 DNA encod
C 426	18	0.9	496	4	AA136894	AA136894 Probe #55	C 499	18	0.9	823	4	AAH03659	AAH03659 Human cdn
C 427	18	0.9	496	4	AAK03082	AAK03082 Human bon	C 500	18	0.9	835	4	AA121073	AA121073 Human bra
C 428	18	0.9	496	4	AAK05386	AAK05386 Human bra	C 501	18	0.9	839	6	ABK79237	ABK79237 Bacillus
C 429	18	0.9	496	4	ABE30660	ABE30660 Human l1v	C 502	18	0.9	847	5	AAE75431	AAE75431 DNA encod
C 430	18	0.9	496	6	ABE05731	ABE05731 Human gen	C 503	18	0.9	847	5	AAE90911	AAE90911 DNA encod
C 431	18	0.9	498	10	ADK76237	ADK76237 Human BSK	C 504	18	0.9	853	3	AAE48249	AAE48249 Arabidops
C 432	18	0.9	508	9	ACLI6737	ACLI6737 DNA clone	C 505	18	0.9	854	6	ABZ14401	ABZ14401 Arabidops
C 433	18	0.9	511	4	AA120967	AA120967 Probe #10	C 506	18	0.9	861	4	AA167448	AA167448 Nucleotid
C 434	18	0.9	511	4	AA122936	AA122936 Probe #12	C 507	18	0.9	890	12	ACH87267	ACH87267 Human gen
C 435	18	0.9	511	4	ABE68026	ABE68026 Human foe	C 508	18	0.9	903	3	AAE52125	AAE52125 Arabidops
C 436	18	0.9	511	4	ABE66036	ABE66036 Human foe	C 509	18	0.9	977	3	AAE94487	AAE94487 DNA encod
C 437	18	0.9	511	4	AA148232	AA148232 Probe #16	C 510	18	0.9	1002	5	AAE27039	AAE27039 Rice caif
C 438	18	0.9	511	4	AA146214	AA146214 Probe #14	C 511	18	0.9	1008	10	AD196481	AD196481 Rice caif
C 439	18	0.9	511	4	ABE48160	ABE48160 Human bra	C 512	18	0.9	1008	12	ADK69726	ADK69726 C. neofo
C 440	18	0.9	511	4	ABE50088	ABE50088 Human bra	C 513	18	0.9	1014	10	ADA56193	ADA56193 Gene enco
C 441	18	0.9	511	4	ABE33121	ABE33121 Probe #11	C 514	18	0.9	1092	5	AAE82624	AAE82624 DNA encod
C 442	18	0.9	511	4	ABE35064	ABE35064 Probe #13	C 515	18	0.9	1102	5	AAE51701	AAE51701 DNA encod
C 443	18	0.9	511	4	AAK40199	AAK40199 Human bon	C 516	18	0.9	1110	6	ABQ92553	ABQ92553 Human sec
C 444	18	0.9	511	4	AAK42167	AAK42167 Human bon	C 517	18	0.9	1110	8	ADA40004	ADA40004 Human sec
C 445	18	0.9	511	4	AAK14460	AAK14460 Human bra	C 518	18	0.9	1110	10	ADA56193	ADA56193 Gene enco
C 446	18	0.9	511	4	AAK16420	AAK16420 Human bra	C 519	18	0.9	1116	12	AD128114	AD128114 Human cdn
C 447	18	0.9	511	4	ABE41777	ABE41777 Human l1v	C 520	18	0.9	1126	4	AAE58605	AAE58605 Human REC
C 448	18	0.9	511	4	ABE39779	ABE39779 Human l1v	C 521	18	0.9	1131	2	AAV84367	AAV84367 Human sto
C 449	18	0.9	511	5	AA106680	AA106680 Probe #66	C 522	18	0.9	1143	1	AAE90961	AAE90961 Promoter
C 450	18	0.9	511	5	AA108599	AA108599 Probe #85	C 523	18	0.9	1147	4	AAK51687	AAK51687 Human pol
C 451	18	0.9	511	6	ABE16216	ABE16216 Human gen	C 524	18	0.9	1149	4	AAE54496	AAE54496 Botulism
C 452	18	0.9	511	6	ABE16216	ABE16216 Human gen	C 525	18	0.9	1153	6	ABQ34659	ABQ34659 Oligonuc1
C 453	18	0.9	521	9	ABE63287	ABE63287 Rat seque	C 526	18	0.9	1153	6	ABQ34658	ABQ34658 Oligonuc1
C 454	18	0.9	521	10	ADK57574	ADK57574 Toxicity- r	C 527	18	0.9	1161	4	AAQ34677	AAQ34677 Probe of
C 455	18	0.9	521	10	ADK57574	ADK57574 Toxicity- r	C 528	18	0.9	1161	4	AB107605	AB107605 Drosoph1l
C 456	18	0.9	529	9	AAE44402	AAE44402 Arabidops	C 529	18	0.9	1215	6	ABE52838	ABE52838 Oligonuc1
C 457	18	0.9	537	9	ACLI2472	ACLI2472 DNA clone	C 530	18	0.9				
C 458	18	0.9	537	9	ACLI2472	ACLI2472 DNA clone	C 531	18	0.9				
C 459	18	0.9	538	2	AAE59345	AAE59345 Mouse NTR	C 532	18	0.9				

533	18	0.9	1215	6	AB052839	Abq52839 Oligonuc1	C 606	18	0.9	2431	6	ABN95768	Abn95768 Gene #226
534	18	0.9	1239	3	AA046261	Aac46261 Arabidops	C 607	18	0.9	2431	11	AD131872	Ad131872 Human cDN
535	18	0.9	1239	3	AA032853	Aac32853 Arabidops	C 608	18	0.9	2433	8	ADA70969	Ada70969 Rice gene
536	18	0.9	1272	3	ADA48527	Ada48527 Rice gene	C 609	18	0.9	2453	4	AB122256	Ab122256 Drosophill
537	18	0.9	1276	3	AA15086	Aa15086 Transcript	C 610	18	0.9	2454	4	AAH77922	Aah77922 Nucleotid
538	18	0.9	1295	8	ACA32245	Aca32245 Prokaryot	C 611	18	0.9	2505	8	AB223069	Ab223069 Human GPC
539	18	0.9	1321	12	AD074449	Ad074449 Human ova	C 612	18	0.9	2559	12	AD002358	Ad002358 Thalecres
540	18	0.9	1360	1	AA087072	Aa087072 Rpt-1 cto	C 613	18	0.9	2564	5	AB121816	Ab121816 Drosophill
541	18	0.9	1376	4	AA080815	Aa080815 Mammalian	C 614	18	0.9	2599	5	AB14651	Ab14651 Human ner
542	18	0.9	1390	2	AAV84524	Aav84524 Human sec	C 615	18	0.9	2610	10	ADD55878	Add55878 Thalecres
543	18	0.9	1390	4	ABA83307	Ab83307 Human sec	C 616	18	0.9	2633	5	ABA20784	Ab20784 Human Cen
544	18	0.9	1390	9	ACH04808	Ach04808 Novel hum	C 617	18	0.9	2633	12	ADN41798	Adn41798 Novel hum
545	18	0.9	1390	9	ACD44618	Acd44618 Human cDN	C 618	18	0.9	2682	2	AAQ39212	Aaq39212 CENP-B CD
546	18	0.9	1392	3	AA050457	Aac050457 Arabidops	C 619	18	0.9	2682	9	ACA62959	Aca62959 DNA encod
547	18	0.9	1392	3	AD069365	Ad069365 C. neofor	C 620	18	0.9	2738	4	AB108506	Ab108506 Drosophill
548	18	0.9	1393	2	AAQ70103	Aaq70103 Malarial	C 621	18	0.9	2826	3	AA098975	Aa098975 Human pan
549	18	0.9	1420	4	AB110201	Ab110201 Drosophill	C 622	18	0.9	2826	6	AB232643	Ab232643 Candida a
550	18	0.9	1428	3	AAA99466	Aaa99466 Sakuranet	C 623	18	0.9	2829	10	AD036061	Ad036061 C. neofor
551	18	0.9	1452	10	ACC61055	Acc61055 Gene sequ	C 624	18	0.9	3041	12	AD036061	Ad036061 Novel mou
552	18	0.9	1452	10	ADK62761	Adk62761 Disease t	C 625	18	0.9	3098	4	AB106272	Ab106272 Drosophill
553	18	0.9	1457	3	AAA99468	Aaa99468 Sakuranet	C 626	18	0.9	3240	4	AAH14453	Aah14453 Human cDN
554	18	0.9	1473	12	ADK71738	Adk71738 Rice RNA-	C 627	18	0.9	3283	4	AA094567	Aa094567 Human ful
555	18	0.9	1494	8	ADA70445	Ada70445 Rice gene	C 628	18	0.9	3417	4	AAK94567	Aak94567 Human ful
556	18	0.9	1497	4	AA084402	Aa084402 Maize Bx1	C 629	18	0.9	3417	12	ADL31446	Adl31446 Full leng
557	18	0.9	1508	2	AAV07665	Aav07665 Arabidops	C 630	18	0.9	3419	12	ADQ22081	Adq22081 Drosophill
558	18	0.9	1508	2	AA047578	Aa047578 Arabidops	C 631	18	0.9	3615	4	AB120427	Ab120427 Drosophill
559	18	0.9	1513	3	AA039532	Aa039532 Arabidops	C 632	18	0.9	3717	3	AAA64660	Aaa64660 DNA encod
560	18	0.9	1544	4	AB092026	Ab092026 Human slo	C 633	18	0.9	3729	5	AA094337	Aa094337 DNA encod
561	18	0.9	1544	4	AAK52671	Aak52671 Human pol	C 634	18	0.9	3765	4	AB107604	Ab107604 Drosophill
562	18	0.9	1554	6	AB232587	Ab232587 Candida a	C 635	18	0.9	3787	5	AAH81775	Aah81775 Human dif
563	18	0.9	1601	3	AA038735	Aa038735 Arabidops	C 636	18	0.9	3787	10	ADK66981	Adk66981 Gene #71
564	18	0.9	1602	3	AA041493	Aa041493 Arabidops	C 637	18	0.9	3982	12	ADJ67450	Adj67450 Human ova
565	18	0.9	1677	10	ACC61290	Acc61290 Gene sequ	C 638	18	0.9	4055	12	ADU67451	Adu67451 Human ova
566	18	0.9	1677	10	ADK63665	Adk63665 Disease t	C 639	18	0.9	4114	4	AB102938	Ab102938 Drosophill
567	18	0.9	1684	4	AA137453	Aa137453 Human mus	C 640	18	0.9	4257	12	ADU67448	Adu67448 Human ova
568	18	0.9	1684	8	ABX00441	Abx00441 CDNA enc	C 641	18	0.9	4371	3	AAA99469	Aaa99469 Human ova
569	18	0.9	1684	12	ADJ31191	Adj31191 Human mus	C 642	18	0.9	4466	2	AAQ70102	Aaq70102 Malarial
570	18	0.9	1734	4	AAH13812	Aah13812 Human cDN	C 643	18	0.9	5124	4	AA095024	Aa095024 DNA encod
571	18	0.9	1743	3	AA042683	Aa042683 Arabidops	C 644	18	0.9	5734	10	ADU67452	Adu67452 Human ova
572	18	0.9	1800	11	ADP64937	Adp64937 Human cen	C 645	18	0.9	5797	9	ADA20300	Ada20300 Human PTP
573	18	0.9	1800	11	ADP64937	Adp64937 Human cen	C 646	18	0.9	6476	4	AB102797	Ab102797 Drosophill
574	18	0.9	1806	5	AA064443	Aa064443 Arabidops	C 647	18	0.9	6567	12	ADN04071	Adn04071 Human bre
575	18	0.9	1812	10	ACF36554	Acf36554 O. sativa	C 648	18	0.9	6567	12	ADU67447	Adu67447 Antipsoi
576	18	0.9	1832	12	AD126112	Ad126112 Human cDN	C 649	18	0.9	5688	12	ADU67447	Adu67447 Human ova
577	18	0.9	1840	5	ABA20783	Ab20783 Human ner	C 650	18	0.9	5688	12	ADU67452	Adu67452 Human ova
578	18	0.9	1840	12	ADN41799	Adn41799 Rice gene	C 651	18	0.9	5734	10	ADU67452	Adu67452 Human ova
579	18	0.9	1872	8	ADA71079	Ada71079 Arabidops	C 652	18	0.9	5797	9	ADA20300	Ada20300 Human PTP
580	18	0.9	1878	6	AB213608	Ab213608 Arabidops	C 653	18	0.9	6471	4	AB102797	Ab102797 Drosophill
581	18	0.9	1878	6	ADG87846	Adg87846 A. thalia	C 654	18	0.9	6471	4	AB102797	Ab102797 Drosophill
582	18	0.9	1952	4	AAH29727	Aah29727 S. cerevis	C 655	18	0.9	6471	4	AB102797	Ab102797 Drosophill
583	18	0.9	1962	6	AB214737	Ab214737 Arabidops	C 656	18	0.9	6471	4	AB102797	Ab102797 Drosophill
584	18	0.9	1969	11	ADM01444	Adm01444 Human cDN	C 657	18	0.9	6471	4	AB102797	Ab102797 Drosophill
585	18	0.9	1986	4	AA056390	Aa056390 ABC trans	C 658	18	0.9	6471	4	AB102797	Ab102797 Drosophill
586	18	0.9	2000	6	AB216299	Ab216299 Arabidops	C 659	18	0.9	6471	4	AB102797	Ab102797 Drosophill
587	18	0.9	2000	6	ADA69271	Ada69271 Arabidops	C 660	18	0.9	6471	4	AB102797	Ab102797 Drosophill
588	18	0.9	2038	6	ABN95604	Abn95604 Gene #210	C 661	18	0.9	6471	4	AB102797	Ab102797 Drosophill
589	18	0.9	2067	12	ADM47636	Adm47636 Polynucle	C 662	18	0.9	6471	4	AB102797	Ab102797 Drosophill
590	18	0.9	2071	1	AA090960	Aa090960 Promoter	C 663	18	0.9	6471	4	AB102797	Ab102797 Drosophill
591	18	0.9	2090	12	ADP22429	Adp22429 Sea-sequit	C 664	18	0.9	6471	4	AB102797	Ab102797 Drosophill
592	18	0.9	2093	4	AA159106	Aa159106 Human pol	C 665	18	0.9	6471	4	AB102797	Ab102797 Drosophill
593	18	0.9	2093	5	AD099329	Ad099329 DNA encod	C 666	18	0.9	6471	4	AB102797	Ab102797 Drosophill
594	18	0.9	2093	5	ADB49089	Adb49089 Novel hum	C 667	18	0.9	6471	4	AB102797	Ab102797 Drosophill
595	18	0.9	2102	10	ADB63120	Adb63120 Human cDN	C 668	18	0.9	6471	4	AB102797	Ab102797 Drosophill
596	18	0.9	2124	4	AA054915	Aa054915 Nucleotid	C 669	18	0.9	6471	4	AB102797	Ab102797 Drosophill
597	18	0.9	2132	4	AA067151	Aa067151 Arabidops	C 670	18	0.9	6471	4	AB102797	Ab102797 Drosophill
598	18	0.9	2135	3	AAA57881	Aaa57881 Arabidops	C 671	18	0.9	6471	4	AB102797	Ab102797 Drosophill
599	18	0.9	2159	2	AAV07667	Aav07667 Maize DIM	C 672	18	0.9	6471	4	AB102797	Ab102797 Drosophill
600	18	0.9	2169	10	AD157346	Ad157346 Human PYR	C 673	18	0.9	6471	4	AB102797	Ab102797 Drosophill
601	18	0.9	2195	3	AB123278	Ab123278 Drosophill	C 674	18	0.9	6471	4	AB102797	Ab102797 Drosophill
602	18	0.9	2345	4	AA047265	Aa047265 Arabidops	C 675	18	0.9	6471	4	AB102797	Ab102797 Drosophill
603	18	0.9	2355	12	ADQ24169	Adq24169 Human sof	C 676	18	0.9	6471	4	AB102797	Ab102797 Drosophill
604	18	0.9	2406	4	AB130485	Ab130485 Drosophill	C 677	18	0.9	6471	4	AB102797	Ab102797 Drosophill
605	18	0.9	2415	6	ABK98553	Abk98553 Botulinum	C 678	18	0.9	6471	4	AB102797	Ab102797 Drosophill

C 679	18	0.9	7808	12	ADJ88338	C 752	17	0.9	46	12	ADH69917	Adi69917 Human Vbe
C 680	18	0.9	7808	12	ADP57720	C 753	17	0.9	51	3	AAA77472	Aaa77472 Human ubi
C 681	18	0.9	7812	12	ADP21334	C 754	17	0.9	51	3	AAA77468	Aaa77468 Human ubi
C 682	18	0.9	7827	6	ABZ53311	C 755	17	0.9	51	3	AAA77475	Aaa77475 Human ubi
C 683	18	0.9	7847	11	ADM29295	C 756	17	0.9	51	3	AAA77471	Aaa77471 Human ubi
C 684	18	0.9	8307	4	ABL23161	C 757	17	0.9	51	3	AAA77474	Aaa77474 Human ubi
C 685	18	0.9	8438	2	AAQ73500	C 758	17	0.9	51	3	AAA77470	Aaa77470 Human ubi
C 686	18	0.9	9291	4	ABL20426	C 759	17	0.9	51	3	AAA77469	Aaa77469 Human ubi
C 687	18	0.9	9522	10	ADN97063	C 760	17	0.9	65	6	ABN46076	Abn46076 Human sp1
C 688	18	0.9	9522	10	ADN99110	C 761	17	0.9	90	4	AA523671	AA523671 Tetracycl
C 689	18	0.9	10079	2	AAQ88057	C 762	17	0.9	94	3	AAA36682	AAA36682 RSV and p
C 690	18	0.9	10079	2	AAI92317	C 763	17	0.9	94	3	ACH89206	Ach89206 Human gen
C 691	18	0.9	10079	3	AAA82894	C 764	17	0.9	98	12	ACH894145	ACH894145 Human gen
C 692	18	0.9	10079	10	ADL13925	C 765	17	0.9	100	8	ACD79044	AcD79044 E. coli K
C 693	18	0.9	10079	11	ADM15669	C 766	17	0.9	104	3	AAC24011	Aac24011 Human sec
C 694	18	0.9	10079	12	ADQ05100	C 767	17	0.9	105	2	AAV55843	AAV55843 Pro-ala m
C 695	18	0.9	11157	5	ABA82023	C 768	17	0.9	107	4	AAH62839	AAH62839 Shrimp wh
C 696	18	0.9	11331	5	ABA85696	C 769	17	0.9	108	4	AAK58644	AAK58644 Human imm
C 697	18	0.9	11597	4	ABL23160	C 770	17	0.9	108	4	AAK58644	AAK58644 Human imm
C 698	18	0.9	12124	2	AAV62854	C 771	17	0.9	117	4	AAI25222	AAI25222 Probe #15
C 699	18	0.9	12124	2	AAV61625	C 772	17	0.9	117	4	AAI25222	AAI25222 Probe #15
C 700	18	0.9	12374	10	ADG66480	C 773	17	0.9	117	4	ABA71012	ABA71012 Human foe
C 701	18	0.9	13329	5	AA571562	C 774	17	0.9	117	4	AAI51214	AAI51214 Probe #15
C 702	18	0.9	14770	6	ABL61893	C 775	17	0.9	117	4	AAK45261	AAK45261 Human bra
C 703	18	0.9	14770	6	ABL68257	C 776	17	0.9	117	4	AAK45261	AAK45261 Human bra
C 704	18	0.9	14770	6	ABL68538	C 777	17	0.9	117	4	ABSA4936	ABSA4936 Human liv
C 705	18	0.9	14770	10	ADH31314	C 778	17	0.9	118	4	AAI54991	AAI54991 Human foe
C 706	18	0.9	14797	5	AA565159	C 779	17	0.9	118	4	ABAT74515	ABAT74515 Human foe
C 707	18	0.9	15187	5	AA586131	C 780	17	0.9	118	4	ABAT74515	ABAT74515 Human foe
C 708	18	0.9	15439	5	AA586131	C 781	17	0.9	118	4	AAK49158	AAK49158 Human bra
C 709	18	0.9	15439	5	AA529744	C 782	17	0.9	118	4	AAK49158	AAK49158 Human bra
C 710	18	0.9	15439	9	ADA27276	C 783	17	0.9	121	6	ABO97104	ABO97104 Mouse ES
C 711	18	0.9	15439	10	ADA12879	C 784	17	0.9	126	10	ACAS5929	ACAS5929 Human sig
C 712	18	0.9	16556	8	AA501807	C 785	17	0.9	126	10	ADIS5725	ADIS5725 Human pol
C 713	18	0.9	17073	8	ABL19434	C 786	17	0.9	128	4	AAI25645	AAI25645 Human foe
C 714	18	0.9	19209	4	AAK86103	C 787	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 715	18	0.9	19209	4	AAK70154	C 788	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 716	18	0.9	24843	6	AA517764	C 789	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 717	18	0.9	37426	10	ABX74421	C 790	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 718	18	0.9	42324	4	AAK84724	C 791	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 719	18	0.9	48908	4	AAK83338	C 792	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 720	18	0.9	49909	2	AAZ23896	C 793	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 721	18	0.9	49909	2	AAZ23891	C 794	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 722	18	0.9	63155	10	ADG85996	C 795	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 723	18	0.9	67191	10	ADG82903	C 796	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 724	18	0.9	67191	10	ADG82903	C 797	17	0.9	128	4	ABAT71933	ABAT71933 Human foe
C 725	18	0.9	67191	11	ADL95495	C 798	17	0.9	130	2	AAV55841	AAV55841 Gly-ala m
C 726	18	0.9	67191	11	ADL95495	C 799	17	0.9	130	2	AAV55841	AAV55841 Gly-ala m
C 727	18	0.9	95001	12	ADH56439	C 800	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 728	18	0.9	95591	10	ADG85301	C 801	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 729	18	0.9	96592	9	ADA02822	C 802	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 730	18	0.9	96592	10	ADG82822	C 803	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 731	18	0.9	96592	12	ADG82822	C 804	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 732	18	0.9	98829	9	AAV55116	C 805	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 733	18	0.9	108316	10	ADG87336	C 806	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 734	18	0.9	110000	10	AAI42063	C 807	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 735	18	0.9	110000	4	AAI99682	C 808	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 736	18	0.9	110000	4	AAI99682	C 809	17	0.9	132	4	ABA64474	ABA64474 Human foe
C 737	18	0.9	113585	12	ADU19197	C 810	17	0.9	142	3	AAI21654	AAI21654 Human sec
C 738	18	0.9	125515	10	ADL11941	C 811	17	0.9	147	4	AAK66682	AAK66682 Human imm
C 739	18	0.9	137560	12	ADP74816	C 812	17	0.9	152	5	AAV55842	AAV55842 Gly-ala m
C 740	18	0.9	143306	8	ABK49586	C 813	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 741	18	0.9	143306	8	ABK49586	C 814	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 742	18	0.9	174566	12	ADL08118	C 815	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 743	18	0.9	186528	6	ABQ75562	C 816	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 744	18	0.9	188888	6	ABQ75562	C 817	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 745	18	0.9	216215	10	ADP69167	C 818	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 746	18	0.9	240000	8	ACD13446	C 819	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 747	18	0.9	349980	6	ABQ81845	C 820	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 748	17	0.9	24	6	ABF42164	C 821	17	0.9	156	4	AAV55842	AAV55842 Gly-ala m
C 749	17	0.9	25	9	ACI52085	C 822	17	0.9	157	4	ABAT74367	ABAT74367 Human foe
C 750	17	0.9	36	12	ADM15529	C 823	17	0.9	157	4	ABAT74367	ABAT74367 Human foe
C 751	17	0.9	39	12	ADH70009	C 824	17	0.9	157	4	AAI54832	AAI54832 Probe #23

825	17	0.9	157	4	ABA39280	Abp39280 Probe #17	C 898	17	0.9	242	4	ABA48792	Abp48792 Human bre
826	17	0.9	157	4	AAK49004	Aak49004 Human bon	C 899	17	0.9	242	4	ABA37965	Abp37965 Probe #16
827	17	0.9	157	4	AAK22833	Aak22833 Human bra	C 900	17	0.9	242	4	ABA33768	Abp33768 Probe #12
828	17	0.9	157	4	ABSA2865	Abp2865 Human liv	C 901	17	0.9	242	4	AAK46439	Aak46439 Human bon
829	17	0.9	157	6	ABSA22640	Abp22640 Human gen	C 902	17	0.9	242	4	AAK40862	Aak40862 Human bon
830	17	0.9	166	6	ABQ96742	Abq96742 Mouse ES	C 903	17	0.9	242	4	AAK15132	Aak15132 Human bra
831	17	0.9	166	12	ACH93320	ACH93320 Human gen	C 904	17	0.9	242	4	AAK20352	Aak20352 Human bra
832	17	0.9	167	6	ABL40825	AbL40825 Human spn	C 905	17	0.9	242	4	ABSA6168	Abp6168 Human liv
833	17	0.9	171	4	ABA72451	AbA72451 Human foe	C 906	17	0.9	242	4	ABSA40439	Abp40439 Human liv
834	17	0.9	171	4	AAI52861	Aai52861 Probe #21	C 907	17	0.9	242	5	AAI07322	Aai07322 Probe #73
835	17	0.9	171	4	AAK47025	Aak47025 Human bon	C 908	17	0.9	242	6	ABSA20764	Abp20764 Human gen
836	17	0.9	171	4	AAK20872	Aak20872 Human bra	C 909	17	0.9	245	4	AAI52374	Aai52374 Probe #21
837	17	0.9	172	4	ABSA46787	Abp46787 Human liv	C 910	17	0.9	245	4	AAK46521	Aak46521 Human bon
838	17	0.9	172	4	AAK55739	Aak55739 Human lmm	C 911	17	0.9	245	4	AAK20397	Aak20397 Human bra
839	17	0.9	174	12	ACH81135	ACH81135 Human gen	C 912	17	0.9	245	4	ABSA6278	Abp6278 Human liv
840	17	0.9	179	6	ABQ98122	Abq98122 Mouse ES	C 913	17	0.9	245	6	ABSA20878	Abp20878 Human gen
841	17	0.9	184	4	AAI20994	Aai20994 Probe #10	C 914	17	0.9	256	10	ACH81394	ACH81394 Human gen
842	17	0.9	184	4	ABSA48184	AbA48184 Human bre	C 915	17	0.9	261	4	AAI19644	Aai19644 Probe #95
843	17	0.9	184	4	AAK40228	Aak40228 Human bon	C 916	17	0.9	261	4	AAI44840	Aai44840 Probe #13
844	17	0.9	184	4	AAK14486	Aak14486 Human bra	C 917	17	0.9	261	4	ABSA6790	Abp6790 Human bre
845	17	0.9	184	6	ABSA71097	Abp71097 Human GPC	C 918	17	0.9	261	4	AAK38836	Aak38836 Human bon
846	17	0.9	184	10	ADD69033	ADD69033 Human Bv8	C 919	17	0.9	261	4	AAK13107	Aak13107 Human bon
847	17	0.9	187	4	AAI24014	Aai24014 Probe #13	C 920	17	0.9	261	4	AAI44840	Aai44840 Probe #10
848	17	0.9	187	4	ABSA69127	Abp69127 Human foe	C 921	17	0.9	261	4	AAK38836	Aak38836 Human bon
849	17	0.9	187	4	AAI49312	Aai49312 Probe #17	C 922	17	0.9	261	4	AAK13107	Aak13107 Human bon
850	17	0.9	187	4	AAK43237	Aak43237 Human bon	C 923	17	0.9	261	4	AAK38836	Aak38836 Human bon
851	17	0.9	187	4	AAK17438	Aak17438 Human bra	C 924	17	0.9	261	4	AAK38836	Aak38836 Human bon
852	17	0.9	187	5	AAI09597	Aai09597 Probe #95	C 925	17	0.9	261	5	AAI05363	Aai05363 Probe #53
853	17	0.9	189	4	AAI25169	Aai25169 Probe #15	C 926	17	0.9	261	6	ABSA12917	Abp12917 Human gen
854	17	0.9	189	4	ABSA70934	Abp70934 Human foe	C 927	17	0.9	261	12	ACH86903	ACH86903 Human gen
855	17	0.9	189	4	AAI51123	Aai51123 Probe #19	C 928	17	0.9	261	12	ADP94049	ADP94049 Cotton ex
856	17	0.9	189	4	ABSA73767	Abp73767 Probe #15	C 929	17	0.9	264	6	ABSA15934	Abp15934 Human ORF
857	17	0.9	189	4	AAK45170	Aak45170 Human bon	C 930	17	0.9	270	6	AAI73119	Aai73119 Cotton tabs
858	17	0.9	189	4	AAK19205	Aak19205 Human bra	C 931	17	0.9	270	6	AAI73119	Aai73119 Cotton tabs
859	17	0.9	189	4	ABSA4842	Abp4842 Human liv	C 932	17	0.9	276	4	AAI20201	Aai20201 Probe #10
860	17	0.9	189	6	ABSA19420	Abp19420 Human gen	C 933	17	0.9	276	4	AAI45401	Aai45401 Probe #14
861	17	0.9	198	4	AAI53415	Aai53415 Probe #22	C 934	17	0.9	276	4	ABSA47345	Abp47345 Human bra
862	17	0.9	198	4	AAK47583	Aak47583 Human bon	C 935	17	0.9	276	4	AAK32331	Aak32331 Probe #10
863	17	0.9	198	4	AAK21422	Aak21422 Human bra	C 936	17	0.9	276	4	AAK32331	Aak32331 Probe #10
864	17	0.9	198	4	ABSA73119	Abp73119 Human liv	C 937	17	0.9	276	4	AAK32331	Aak32331 Probe #10
865	17	0.9	198	4	ACH84117	ACH84117 Human liv	C 938	17	0.9	276	4	AAK32331	Aak32331 Probe #10
866	17	0.9	223	12	ACH84117	ACH84117 Human liv	C 939	17	0.9	276	4	AAK32331	Aak32331 Probe #10
867	17	0.9	225	4	ABSA73861	Abp73861 Human foe	C 940	17	0.9	276	4	AAK32331	Aak32331 Probe #10
868	17	0.9	225	4	AAI54307	Aai54307 Probe #22	C 941	17	0.9	276	4	AAI54307	Aai54307 Probe #22
869	17	0.9	225	4	AAK48479	Aak48479 Human bon	C 942	17	0.9	276	6	ABSA13475	Abp13475 Human liv
870	17	0.9	225	4	AAK48479	Aak48479 Human bon	C 943	17	0.9	276	9	AAI18001	Aai18001 Human sec
871	17	0.9	225	4	AAK22314	Aak22314 Human bra	C 944	17	0.9	280	3	AAK31861	Aak31861 Human sec
872	17	0.9	232	4	ABSA48173	Abp48173 Human liv	C 945	17	0.9	280	3	AAK31861	Aak31861 Human sec
873	17	0.9	232	4	AAI22451	Aai22451 Probe #12	C 946	17	0.9	286	8	ABX48171	ABX48171 Bovine ES
874	17	0.9	232	4	ABSA67527	Abp67527 Human foe	C 947	17	0.9	292	10	ABX86453	ABX86453 Corn ear-
875	17	0.9	232	4	ABSA49623	Abp49623 Human bre	C 948	17	0.9	292	5	AAI28183	Aai28183 DNA encod
876	17	0.9	232	4	AAK43608	Aak43608 Human bon	C 949	17	0.9	292	4	ABSA69302	Abp69302 Human foe
877	17	0.9	232	4	AAK41698	Aak41698 Human bon	C 950	17	0.9	299	4	AAI49470	Aai49470 Probe #18
878	17	0.9	232	4	AAK15953	Aak15953 Human bra	C 951	17	0.9	299	4	ABSA51297	Abp51297 Human bra
879	17	0.9	232	4	ABSA41287	Abp41287 Human liv	C 952	17	0.9	299	4	ABSA51297	Abp51297 Human bra
880	17	0.9	232	6	ABSA15705	Abp15705 Human gen	C 953	17	0.9	299	4	AAK43403	Aak43403 Human bra
881	17	0.9	234	4	AAI21604	Aai21604 Probe #11	C 954	17	0.9	299	4	AAK43403	Aak43403 Human bra
882	17	0.9	234	4	ABSA6681	Abp6681 Human foe	C 955	17	0.9	299	4	AAK43403	Aak43403 Human bra
883	17	0.9	234	4	AAI46893	Aai46893 Probe #15	C 956	17	0.9	299	4	AAK43403	Aak43403 Human bra
884	17	0.9	234	4	ABSA48769	Abp48769 Human bre	C 957	17	0.9	299	5	AAI09746	Aai09746 Probe #97
885	17	0.9	234	4	ABSA3741	Abp3741 Probe #12	C 958	17	0.9	299	6	ABSA17496	Abp17496 Human gen
886	17	0.9	234	4	AAK15107	Aak15107 Human bon	C 959	17	0.9	301	4	AAI19578	Aai19578 Probe #95
887	17	0.9	234	4	AAK15107	Aak15107 Human bon	C 960	17	0.9	301	4	AAI19578	Aai19578 Probe #95
888	17	0.9	234	4	ABSA40416	Abp40416 Human bra	C 961	17	0.9	301	4	AAI44771	Aai44771 Probe #13
889	17	0.9	234	4	ABSA40416	Abp40416 Human bra	C 962	17	0.9	301	4	ABSA46724	Abp46724 Human bra
890	17	0.9	234	4	ABSA40416	Abp40416 Human bra	C 963	17	0.9	301	4	ABSA46724	Abp46724 Human bra
891	17	0.9	234	4	ABSA40416	Abp40416 Human bra	C 964	17	0.9	301	4	ABSA46724	Abp46724 Human bra
892	17	0.9	241	12	ADQ21395	ADQ21395 Human gen	C 965	17	0.9	301	4	AAK38772	Aak38772 Human bon
893	17	0.9	242	4	AAI21627	Aai21627 Probe #11	C 966	17	0.9	301	4	AAK38772	Aak38772 Human bon
894	17	0.9	242	4	ABSA6709	Abp6709 Human foe	C 967	17	0.9	301	5	ABSA38353	Abp38353 Human liv
895	17	0.9	242	4	ABSA71959	Abp71959 Human foe	C 968	17	0.9	301	6	ABSA12847	Abp12847 Human gen
896	17	0.9	242	4	AAI46917	Aai46917 Probe #15	C 969	17	0.9	313	8	ABSA27992	Abp27992 Rice leaf
897	17	0.9	242	4	AAI52322	Aai52322 Probe #21	C 970	17	0.9	314	4	AAI21241	Aai21241 Probe #11

971 17 0.9 314 4 ABa66321 Human foe
 972 17 0.9 314 4 Aa146512 Probe #15
 973 17 0.9 314 4 ABa48424 Human bre
 974 17 0.9 314 4 ABa33385 Probe #11
 975 17 0.9 314 4 AAK40481 Human bon
 976 17 0.9 314 4 AAK14739 Human bra
 977 17 0.9 314 4 ABs40045 Human 1iv
 978 17 0.9 314 5 Aa106950 Probe #69
 979 17 0.9 314 5 ABs14472 Human gen
 980 17 0.9 320 11 AD130833 Human CDN
 981 17 0.9 320 10 ACD96554 Human col
 982 17 0.9 324 6 ABs71103 Human phy
 983 17 0.9 324 10 Aa144331 Human pny
 984 17 0.9 324 10 Aa144331 Human pny
 985 17 0.9 326 4 Aa119635 Human Bv8
 986 17 0.9 326 4 ABa64661 Human toe
 987 17 0.9 326 4 Aa144831 Probe #13
 988 17 0.9 326 4 ABa46781 Human bre
 989 17 0.9 326 4 ABa31785 Probe #10
 990 17 0.9 326 4 AAK38827 Human bon
 991 17 0.9 326 4 AAK13099 Human bra
 992 17 0.9 326 4 ABs38412 Human 1iv
 993 17 0.9 326 5 Aa105354 Probe #53
 994 17 0.9 326 5 ABs12908 Human gen
 995 17 0.9 331 5 Adm19246 Novel hum
 996 17 0.9 333 12 ACh80520 Human gen
 997 17 0.9 334 3 AAc76758 Human ORF
 998 17 0.9 336 6 ABq86023 Arabidops
 999 17 0.9 337 3 AaF09102 Fusaarium
 1000 17 0.9 337 4 Aa146272 Probe #14

ALIGNMENTS

RESULT 1
 ID AAF77094 standard; DNA; 1944 BP.
 AC AAF77094;
 XX 17-MAY-2001 (first entry)
 DT
 DE Brassica napus PERK1 DNA.
 XX
 KM Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
 XX
 CS Brassica napus.
 XX
 EN WO200114563-A1.
 XX
 PD 01-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-CA000966.
 XX
 PR 19-AUG-1999; 99US-0148466P.
 XX
 PR 13-OCT-1999; 99US-0159122P.
 XX
 PA (GORI/) GORING D.
 XX
 PA (SILV/) SILVA N.
 XX
 PI Goring D, Silva N;
 XX
 DR WPI; 2001-244305/25.
 XX
 PT New proline-rich, extensin-like receptor kinase nucleic acids and
 PT polypeptides useful for increasing plant wounding or pathogen resistance,
 PT or for producing transgenic plants with increased wounding or pathogen
 PT resistance.
 XX
 PS Claim 6; Fig 1; 91pp; English.
 XX
 CC The present invention relates to proline-rich extensin-like receptor

CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
 CC increasing the resistance of plants to wounding and pathogens. These are
 CC also useful for producing transgenic plants with increased wounding and
 CC pathogen resistance compared with a wild type plant, as well as in assays
 CC for identifying and developing compounds to inhibit and/or enhance
 CC polypeptide function directly

SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

Query Match 100.0%; Score 1944; DB 4; Length 1944;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCCTCGGCGCGCTCTCGGAGTGTGCTCTCCATCTCCATCAAACTCCACA 60
 1 ATGTCCTCGGCGCGCTCTCGGAGTGTGCTCTCCATCTCCATCAAACTCCACA 60
 Db 1 ATGTCCTCGGCGCGCTCTCGGAGTGTGCTCTCCATCTCCATCAAACTCCACA 60
 QY 61 ACCACGACTCTCTCTCCAGCTTCCGCTCTCCGACACACCTCTCTCTCCGCG 120
 61 ACCACGACTCTCTCTCCAGCTTCCGCTCTCCGACACACCTCTCTCTCCGCG 120
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 121 CCATCCACTATTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 Db 121 CCATCCACTATTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 QY 181 CCATCTCCACCACTCCATCTACGCGGATCTCCACCTCTCTCTCTCTCTCTCT 240
 181 CCATCTCCACCACTCCATCTACGCGGATCTCCACCTCTCTCTCTCTCTCTCT 240
 Db 181 CCATCTCCACCACTCCATCTACGCGGATCTCCACCTCTCTCTCTCTCTCTCT 240
 QY 241 CCGCTCTCCACTCTGCGCGGATCTCCACCGGACCTCTCTCTCTCTCTCTCTCT 300
 241 CCGCTCTCCACTCTGCGCGGATCTCCACCGGACCTCTCTCTCTCTCTCTCTCT 300
 Db 241 CCGCTCTCCACTCTGCGCGGATCTCCACCGGACCTCTCTCTCTCTCTCTCTCT 300
 QY 301 CCACCTTCAGTCCAGGACCGGATCTCCATCTCTCCAGGAGATCTCTCGACT 360
 301 CCACCTTCAGTCCAGGACCGGATCTCCATCTCTCCAGGAGATCTCTCGACT 360
 Db 301 CCACCTTCAGTCCAGGACCGGATCTCCATCTCTCCAGGAGATCTCTCGACT 360
 QY 361 CCATCT 420
 361 CCATCT 420
 Db 361 CCATCT 420
 QY 421 GGAATGCGCATCGGAGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
 421 GGAATGCGCATCGGAGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
 Db 421 GGAATGCGCATCGGAGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
 QY 481 AAGAAGAAACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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 721 TACTGAGACCGTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
 Db 721 TACTGAGACCGTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
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 781 AGCATTTCACATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 781 AGCATTTCACATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 841 TTAGGACAAAGGCGGTCTGTTAGCTGCAAAAGTGTGTCTCTCTCTCTCTCTCT 900
 841 TTAGGACAAAGGCGGTCTGTTAGCTGCAAAAGTGTGTCTCTCTCTCTCTCTCT 900
 Db 841 TTAGGACAAAGGCGGTCTGTTAGCTGCAAAAGTGTGTCTCTCTCTCTCTCTCT 900

QY 901 GCTGTGAGAGCATTTGAAAGTTGGAGTGTGAGGAGAGAGGAGTTTCAGGAGAGGTT 960
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 QY 1141 GCTAAAGACCTTCTTATCTTCATGAAGATTGCAATCTTAAATCATTCACCGTGATTC 1200
 Db 1141 GCTAAAGACCTTCTTATCTTCATGAAGATTGCAATCTTAAATCATTCACCGTGATTC 1200
 QY 1201 AAGGCTTCAACATATGATGATGATTGCAAGTTGAAGCTTAAGGTTGCTGATTTGGTCTT 1260
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 QY 1261 GCTAAGATTGCTTCTGATACAAACGCAATGATCAACGCTGATGAGGAACTTTGGG 1320
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 QY 1321 TACTTGCTCCGGAATACGCTGCAAGCGGAAAGCTCAGAGAACTGTAAGCTTTTCTCA 1380
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 Db 1381 TTTGGCGTTGCTTTTGGAGCTCATTAATGAGCTGCAACCGGTTGATGCCAATGTC 1440
 QY 1441 TATGTAGATGACAGCTTATGTTGAGGAGGAGCAATGCTTAAACGAGCATCTGAGCA 1500
 Db 1441 TATGTAGATGACAGCTTATGTTGAGGAGGAGCAATGCTTAAACGAGCATCTGAGCA 1500
 QY 1501 GGAGACTTTGAGGGTTTACCTGATGCAAGATGAATGAGTATGAGCAGAGAGAGATG 1560
 Db 1501 GGAGACTTTGAGGGTTTACCTGATGCAAGATGAATGAGTATGAGCAGAGAGAGATG 1560
 QY 1561 GCTGGCAGTGTGCTTGTGCTGCGGCTGTGTTGCCATTGAGCTGCGGAGACCTTGC 1620
 Db 1561 GCTGGCAGTGTGCTTGTGCTGCGGCTGTGTTGCCATTGAGCTGCGGAGACCTTGC 1620
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 Db 1621 ATGAGCCAGATTGTGCGTGCCTTAGAGAGAAATGATCACTGTGATCTTAAACGAAAGG 1680
 QY 1681 ATGAGACCAAGTCAAAAGCAATGTATACAGCTCATACGAGAGAGACCGATTATGACTCG 1740
 Db 1681 ATGAGACCAAGTCAAAAGCAATGTATACAGCTCATACGAGAGAGACCGATTATGACTCG 1740
 QY 1741 AGCCAGTCAATGAAAGATGAAGAAATTTAGAAAATGCGACTTGAACCTAAGAGTAC 1800
 Db 1741 AGCCAGTCAATGAAAGATGAAGAAATTTAGAAAATGCGACTTGAACCTAAGAGTAC 1800
 QY 1801 AACGCCACGGGTGAGTACAGTAAATCCGACAGTGAATGAGCTGATCCGCTGTGGTTCA 1860
 Db 1801 AACGCCACGGGTGAGTACAGTAAATCCGACAGTGAATGAGCTGATCCGCTGTGGTTCA 1860
 QY 1861 AGCAGCGAGGGCCAAACCAACGCGGAATGAGATGGGAAAGATTAAAGAACCGGTCAG 1920
 Db 1861 AGCAGCGAGGGCCAAACCAACGCGGAATGAGATGGGAAAGATTAAAGAACCGGTCAG 1920
 QY 1921 GGTTATAGTGAACCTTCTCTTAA 1944
 Db 1921 GGTTATAGTGAACCTTCTCTTAA 1944

RESULT 2
 ID ACF36548 standard; cDNA; 1944 BP.
 XX ACF36548;
 AC ACF36548;
 XX 18-DEC-2003 (first entry)
 DT
 DE B. napus PERK1 receptor kinase encoding cDNA.
 XX
 KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
 XX wound; pathogen resistance; plant growth; seed production; gene; ss.
 OS Brassica napus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1944
 FT /tag=a
 FT /transl_except=(pos: 1332..1334, aa: Phe)
 FT /product="PERK1"
 XX /note="Proline-rich Extensin-like Receptor Kinase"
 PN MO2003072763-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 28-FEB-2003; 2003WO-CA000274.
 XX
 PR 28-FEB-2002; 2002CA-02373903.
 PR 28-FEB-2002; 2002US-00086464.
 XX
 PA (GORI/) GORING D.
 PA (SILV/) SILVA N.
 PA (HAFF/) HAFANI Y Z.
 PI Goring D, Silva N, Hafani YZ;
 XX
 DR WPI; 2003-712727/67.
 DR P-PSDB; ABR82937.
 XX
 PT Producing a transgenic plant having an increased plant resistance, plant
 PT growth or seed production comprises transforming a plant with a nucleic
 PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
 PT activity.
 PS
 XX
 PS Claim 3; Fig 1A; 123pp; English.
 CC The invention relates to producing a transgenic plant having increased
 CC plant height, number of branches, number of seed pods and/or seed
 CC production compared to a non-transgenic plant, and/or quicker flowering
 CC or later senescence compared to a non-transgenic plant. The method
 CC involves transforming a plant with a vector including a Proline-rich
 CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
 CC acid molecule having PERK activity. The method, as well as the PERK
 CC nucleic acid molecule and polypeptide, are useful in increasing plant
 CC resistance to wounding and pathogens and in increasing plant growth and
 CC seed production. The nucleic acid molecule and polypeptide may also be
 CC used in producing transgenic plants or transgenic host cells. The present
 CC sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
 CC polypeptide
 XX
 SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1944; DB 10; Length 1944;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTCTCGGCGCGTCTCCGGAGACTGGTTGCGCTCATCTCCACATCAAACTCCACA 60
 Db 1 ATGTCTCGGCGCGTCTCCGGAGACTGGTTGCGCTCATCTCCACATCAAACTCCACA 60
 QY 61 ACCACCACTCTCTCTCAAGCTTCGCTCTCTCTCCACCAACCTTCTTCTCTCGCGCG 120

PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
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PR 14-MAY-1999; 99US-0134221P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 2.4%; Score 47; DB 3; Length 2324;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 GCTTGTGTTGCGCATTCAGCTGCGCGACGACCTTCGATGAGCAGAT 1631
DB 1700 GCTTGTGTTGCGCATTCAGCTGCGCGACGACCTTCGATGAGCAGAT 1746

RESULT 6
ADK53814
ID ADK53814 standard; DNA; 685 BP.
XX
AC ADK53814;
DT 06-MAY-2004 (first entry)
DE
XX
XX Plant DNA sequence which confers altered metabolic characteristic #1197.
XX
KM altered metabolic characteristic; plant; acid metabolism;
KM alcohol metabolism; fatty acid metabolism;
KM branched fatty acid metabolism; alkaloid metabolism;
KM amino acid metabolism; ester metabolism; glyceride metabolism;
KM phenolic metabolism; carbohydrate metabolism; steroid metabolism;
KM terpene metabolism; isoprenoid metabolism; alkene metabolism;
KM alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KM quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
OS Unidentified.
XX
XX WO2003020936-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027884.
XX
XX 31-AUG-2001; 2001US-0316471P.
XX
XX (DOMC ) DOM CHEM CO.
XX (DOMC ) DOM AGRSCIENCES LLC.
XX
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX Oriole JVB, Croesley R, Reddy AS, Shukla V, Larrina I, Miller BA;
XX
XX WPI, 2003-313091/30.
XX
XX Novel genes that confer altered metabolic characteristics in Nicotiana
XX benhamiana plants, useful for altering the levels of metabolites e.g.
XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and steroids.
XX

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PS Claim 1; SEQ ID NO 1197; 2576bp; English.
XX
XX The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC altered glyceride metabolism, altered steroid, oxygenated terpene, or
CC carbohydrate metabolism, altered phenolic metabolism, altered
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.
XX
XX Sequence 685 BP; 181 A; 130 C; 176 G; 197 T; 0 U; 1 Other;

Query Match 1.4%; Score 27; DB 10; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 CTCATTGGCGTTGTCCTTTTGAGCT 1403
DB 461 CTCATTGGCGTTGTCCTTTTGAGCT 487

RESULT 7
ACF36555
ID ACF36555 standard; DNA; 1515 BP.
XX
AC ACF36555;
DT 18-DEC-2003 (first entry)
DE
XX
XX Z. mays PERK protein encoding genomic DNA.
XX
XX PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
XX wound; pathogen resistance; plant growth; seed production; maize; gene;
XX ds.
XX
XX Zea mays.
XX
XX WO2003072763-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-CA000274.
XX
XX 28-FEB-2002; 2002CA-02373903.
XX
XX 28-FEB-2002; 2002US-0008464.
XX
XX (GORI/) GORING D.
XX (SILV/) SILVA N.
XX (HAF/) HAFANI Y Z.
XX
XX Goring D, Silva N, Hafani YZ;
XX
XX WPI, 2003-712727/67.
XX
XX Producing a transgenic plant having an increased plant resistance, plant
XX growth or seed production comprises transforming a plant with a nucleic
XX acid molecule having a Proline-rich Extensin-like Receptor Kinase
XX activity.
XX
XX Disclosure; Fig 21b; 123bp; English.
XX
XX The invention relates to producing a transgenic plant having increased
XX plant height, number of branches, number of seed pods and/or seed
XX production compared to a non-transgenic plant, and/or quicker flowering
XX or later senescence compared to a non-transgenic plant. The method
XX involves transforming a plant with a vector including a Proline-rich
XX Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
XX

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CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents a Z. mays PERK protein encoding genomic DNA (TIGR
CC Accession No. AY108241)
XX

SQ Sequence 1515 BP; 400 A; 330 C; 381 G; 404 T; 0 U; 0 Other;

Query Match
Best Local Similarity 1.3%; Score 26; DB 10; Length 1515;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTTGAGCTAAGTTCCTGATTTTGG 1256
DB 601 TTTGAGCTAAGTTCCTGATTTTGG 626

RESULT 8

AAF22305_06/c
Continuation (7 of 11) of AAF22305 from base 600001 (Arabidopsis thaliana chromosome 4 c
WP Sequence split into 11 fragments LOCUS AAF22305 Accession Aaf22305

WP	Fragment Name	Begin	End
WP	AAF22305_00	1	110000
WP	AAF22305_01	100001	210000
WP	AAF22305_02	200001	310000
WP	AAF22305_03	300001	410000
WP	AAF22305_04	400001	510000
WP	AAF22305_05	500001	610000
WP	AAF22305_06	600001	710000
WP	AAF22305_07	700001	810000
WP	AAF22305_08	800001	910000
WP	AAF22305_09	900001	1010000
WP	AAF22305_10	1000001	1082138

Query Match
Best Local Similarity 1.3%; Score 26; DB 3; Length 110000;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1036 CTGTCTATGAGTTGTTCTTAACAA 1061
DB 109643 CTGTCTATGAGTTGTTCTTAACAA 109618

RESULT 9

AAF22305_07/c
Continuation (8 of 11) of AAF22305 from base 700001 (Arabidopsis thaliana chromosome 4 c
WP Sequence split into 11 fragments LOCUS AAF22305 Accession Aaf22305

WP	Fragment Name	Begin	End
WP	AAF22305_00	1	110000
WP	AAF22305_01	100001	210000
WP	AAF22305_02	200001	310000
WP	AAF22305_03	300001	410000
WP	AAF22305_04	400001	510000
WP	AAF22305_05	500001	610000
WP	AAF22305_06	600001	710000
WP	AAF22305_07	700001	810000
WP	AAF22305_08	800001	910000
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Query Match
Best Local Similarity 1.3%; Score 26; DB 3; Length 110000;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1036 CTGTCTATGAGTTGTTCTTAACAA 1061
DB 9643 CTGTCTATGAGTTGTTCTTAACAA 9618

RESULT 10
ADA70853/c

ID ADA70853 standard; DNA; 1389 BP.

XX ADA70853;

AC 20-NOV-2003 (first entry)

DT 20-NOV-2003 (first entry)

DE Rice gene, SEQ ID 4176.

KW Plant; bacterial infection; fungal infection; viral infection; rice;

XX gene; ds.

OS Oryza sativa.

PN WO2003000898-A1.

XX 03-JAN-2003.

PD 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

PR 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

PI Katagiri F, Quan S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to

PT pathogenic infection for conferring resistance or tolerance to a plant to

PT gene expression.

XX Claim 6; SEQ ID NO 4176; 899bp; English.

PS The present invention relates to a method (M1) for identifying genes

CC involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to

CC expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,

CC or in a corresponding incompatible or compatible interaction. (M1) is

CC useful for conferring resistance to resistance or tolerance to a plant to

CC bacterial, fungal or viral infection. The present sequence was used to

XX illustrate the invention.

SQ Sequence 1389 BP; 412 A; 278 C; 406 G; 293 T; 0 U; 0 Other;

Query Match
Best Local Similarity 1.2%; Score 24; DB 8; Length 1389;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 CCTTCCTCACCCTCACCACCGCCT 693
DB 115 CCTTCCTCACCCTCACCACCGCCT 92

RESULT 11
ADA27371
ID ADA27371 standard; DNA; 1515 BP.
AC ADA27371;
XX 20-NOV-2003 (first entry)
DT 20-NOV-2003 (first entry)
DE HIV-16 L1 codon optimised DNA sequence SEQ ID NO:1.
XX cell line; American Type Culture Collection PTA-4047; ATCC-4047;
XX baculoviruses; viral recombinant protein; virus-like particle; vaccine;
XX diagnostic reagent; human papillomavirus type 16; HPV-16; D1; gene; ds.
OS Synthetic.
OS Human papillomavirus type 16.

```
XX Key Location/Qualifiers
FH 1..1515
FT CDS
FT /tag= a
FT /product= "HPV-16 L1 protein"
FT /transl_except= (pos:208..210,aa:Tyr)
FT /transl_except= (pos:295..297,aa:Val)
XX WO2003068904-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-US004516.
XX
XX 14-FEB-2002; 2002US-0356113P.
XX 14-FEB-2002; 2002US-0356118P.
XX 14-FEB-2002; 2002US-0356119P.
XX 14-FEB-2002; 2002US-0356123P.
XX 14-FEB-2002; 2002US-0356126P.
XX 14-FEB-2002; 2002US-0356133P.
XX 14-FEB-2002; 2002US-0356135P.
XX 14-FEB-2002; 2002US-0356150P.
XX 14-FEB-2002; 2002US-0356151P.
XX 14-FEB-2002; 2002US-0356152P.
XX 14-FEB-2002; 2002US-0356154P.
XX 14-FEB-2002; 2002US-0356156P.
XX 14-FEB-2002; 2002US-0356157P.
XX 14-FEB-2002; 2002US-0356161P.
XX 14-FEB-2002; 2002US-0356162P.
XX
XX (NOVA-) NOVAVAX INC.
XX
XX Robinson RA;
XX WPI; 2003-646475/61.
XX P-PSDB; ADA27363.
XX
XX New insect cell line designated ATCC PTA-4047, useful for replicating
XX baculoviruses to produce large amounts of recombinant proteins of
XX medical, pharmaceutical and veterinary importance.
XX
XX Claim 10; Fig 1; 63pp; English.
XX
XX The present invention describes a cell line comprising a cell that is a
XX clone, derivative, mutant and/or transfectant of a cell line designated
XX American Type Culture Collection (ATCC) PTA-4047. The cell upon culture
XX grows continuously and retains the identifying characteristics of the
XX cell line designated ATCC-4047. Also described is a process of making a
XX cell line. The insect cell line is useful in replicating baculoviruses,
XX as a host substrate for baculovirus plaque assays, as a source of insect
XX proteins, acts as a depot for cell transfection to produce recombinant
XX baculoviruses, and in expressing viral recombinant proteins and virus-like
XX Extracellular and intracellular viral recombinant proteins and virus-like
XX particles expressed from the cell line are useful as pharmaceutical
XX compositions, vaccines or diagnostic reagents. The present sequence
XX represents a human papillomavirus type 16 (HPV-16) L1 codon optimised
XX sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 24; DB 9; Length 1515;
XX Best Local Similarity 100.0%; Pred. No. 1.3;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
AC ADA92549;
XX
XX 20-NOV-2003 (first entry)
XX
XX HPV-16 L1 codon optimised DNA sequence SEQ ID NO:1.
XX
XX codon optimised; viral capsid protein; virus-like particle; VLP;
XX antigenic; human papillomavirus infection; virucide; vaccine;
XX gene therapy; human papillomavirus type 16; dysplasia; infection; HPV-16;
XX L1; gene; ds.
XX
XX Synthetic;
XX Human papillomavirus type 16.
XX
XX Key Location/Qualifiers
FH 1..1515
FT CDS
FT /tag= a
FT /product= "codon optimised L1 amino acid sequence"
FT /transl_except= (pos:208..210,aa:Tyr)
FT /transl_except= (pos:295..297,aa:Val)
XX
XX WO2003068933-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-US004480.
XX
XX 14-FEB-2002; 2002US-0356113P.
XX 14-FEB-2002; 2002US-0356118P.
XX 14-FEB-2002; 2002US-0356119P.
XX 14-FEB-2002; 2002US-0356123P.
XX 14-FEB-2002; 2002US-0356126P.
XX 14-FEB-2002; 2002US-0356133P.
XX 14-FEB-2002; 2002US-0356135P.
XX 14-FEB-2002; 2002US-0356150P.
XX 14-FEB-2002; 2002US-0356151P.
XX 14-FEB-2002; 2002US-0356152P.
XX 14-FEB-2002; 2002US-0356154P.
XX 14-FEB-2002; 2002US-0356156P.
XX 14-FEB-2002; 2002US-0356157P.
XX 14-FEB-2002; 2002US-0356161P.
XX 14-FEB-2002; 2002US-0356162P.
XX
XX (NOVA-) NOVAVAX INC.
XX
XX Robinson RA;
XX WPI; 2003-689664/65.
XX P-PSDB; ADA92541.
XX
XX New codon optimized polynucleotide encoding a viral capsid protein that
XX self assembles into a virus-like particle, useful for diagnosing,
XX preventing or treating human papillomavirus infections or associated
XX disorders.
XX
XX Claim 7; Page 113; 123pp; English.
XX
XX The present invention describes a codon optimised polynucleotide encoding
XX a viral capsid protein that self assembles into a virus-like particle
XX (VLP) that exhibits conformational antigenic epitopes capable of raising
XX neutralising antibodies, where the VLP is expressed from a host cell
XX extracellularly. Also described: (1) a vector comprising the above codon
XX optimised polynucleotide operably linked to a eukaryotic or prokaryotic
XX regulatory control element, capable of replication in prokaryotic and/or
XX eukaryotic host; (2) a host cell comprising the vector; (3) a
XX pharmaceutical or vaccine composition for treating, ameliorating or
XX preventing a papillomavirus related disease or disorder, comprising a
XX multiplicity of VLPs that exhibit conformational antigenic epitopes, and
XX a carrier, diluent or adjuvant; (4) a diagnostic kit for detecting a
XX papillomavirus infection, comprising a multiplicity of VLPs that exhibit
XX conformational antigenic epitopes, and a detection agent comprising a
XX detectable label; (5) a method for preparing the above codon optimised
XX polynucleotide, comprising replacing codons that are underutilised in
```

CC insect cells with codons that are utilised at high levels in insect
 CC cells, to create an initially-modified nucleotide sequence, and modifying
 CC the initially-modified nucleotide sequence by choosing a preferred codon
 CC for the initially-modified sequence, where the ratio of GC nucleotide
 CC pairs to AT nucleotide pairs in the further-modified nucleotide sequence
 CC trends towards about 1:1, where the number of palindromic and stem-loop
 CC DNA structures in the further-modified nucleotide sequence is minimised,
 CC and where the number of transcription and post-transcription repressor
 CC elements are minimised; and (6) methods for treating, ameliorating or
 CC preventing a papillomavirus related disease or disorder, or for
 CC protecting an individual against a papillomavirus infection, comprising
 CC administering to an individual an amount of the composition or vaccine
 CC cited above. The VLP has virucide activity and can be used in vaccines
 CC and in gene therapy. The composition and methods of the present invention
 CC are useful in diagnosing, preventing or treating human papillomavirus
 CC infections or associated disorders, such as dysplasia. The present
 CC sequence represents an HPV-16 codon optimised LI nucleotide sequence from
 CC the present invention.

CC Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

CC Query Match 1.2%; Score 24; DB 9; Length 1515;

CC Best Local Similarity 100.0%; Pred. No. 1.3;

CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 669 ACCTCTCCACCTCCACCCGCC 692
 DB 1471 ACCTCTCCACCTCCACCCGCC 1494

RESULT 13

ID ADA14298 standard; DNA; 1515 BP.

AC ADA14298;

DT 06-NOV-2003 (first entry)

DE HPV-16 LI codon optimised sequence SEQ ID NO:1.

XX purification; recombinant extracellular virus-like particle;
 KW recombinant intracellular virus-like particle; virus-like particle; VLP;
 KW virucide; vaccine; gene therapy; human papillomavirus; HPV; infection;
 KW dysplasia; HPV-16; LI; codon optimised; gene; ds.

XX Human papillomavirus type 16.

Key Location/Qualifiers

FT CDS

FT 1..1515

FT /*tag= a

FT /product= "HPV-16 LI protein"

FT /transl_except= (pos:208..210,aa:Tyr)

FT /transl_except= (pos:295..297,aa:Val)

XX WO2003068993-A1.

XX 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004474.

PR 14-FEB-2002; 2002US-0356113P.

PR 14-FEB-2002; 2002US-0356118P.

PR 14-FEB-2002; 2002US-0356119P.

PR 14-FEB-2002; 2002US-0356123P.

PR 14-FEB-2002; 2002US-0356126P.

PR 14-FEB-2002; 2002US-0356133P.

PR 14-FEB-2002; 2002US-0356135P.

PR 14-FEB-2002; 2002US-0356150P.

PR 14-FEB-2002; 2002US-0356151P.

PR 14-FEB-2002; 2002US-0356152P.

PR 14-FEB-2002; 2002US-0356154P.

PR 14-FEB-2002; 2002US-0356156P.

PR 14-FEB-2002; 2002US-0356157P.

PR 14-FEB-2002; 2002US-0356161P.
 PR 14-FEB-2002; 2002US-0356162P.
 XX
 XX (NOVA-) NOVAVAX INC.
 XX
 XX Robinson RA, Thompson MM;
 DR WPI; 2003-679645/64.
 DR P-PSDB; ADA14290.

PT Purifying a recombinant human papillomavirus (HPV) LI, useful for
 PT diagnosing, preventing or treating HPV infections, comprises clarifying,
 PT concentrating and diafiltering cells containing HPV particles.

XX Example 4; Fig 1A-C; 111pp; English.

CC The present invention describes a method for purifying a recombinant
 CC extracellular or intracellular virus-like particle (VLP). The method
 CC comprises harvesting a cell suspension comprising cells containing a
 CC plurality of VLPs to produce a harvested supernatant, optionally
 CC disrupting the harvested cells to produce cell lysates containing the
 CC VLP, clarifying the harvested supernatant, concentrating the clarified
 CC supernatant, diafiltering the concentrated supernatant, and recovering
 CC the purified recombinant VLP. Also described: (1) a cell line designated
 CC as Sf-9S deposited as American Type Culture Collection (ATCC) PTA-4047;
 CC (2) producing the cell line described above; (3) host cells that express
 CC one or more recombinant gene products with an enhanced yield; (4)
 CC producing a foreign protein in an insect cell; (5) nucleic acid sequences
 CC that correspond to and code for human papillomavirus (HPV) polypeptides;
 CC and (6) pharmaceutical compositions comprising an amount of the
 CC recombinant viral gene products, VLPs, agonists, antagonists, or the
 CC active fragment of a viral gene product. The VLPs have virucide activity,
 CC and can be used in vaccines and in gene therapy. The method is useful in
 CC isolating and purifying expressed viral gene products, including VLPs, in
 CC vitro. The gene products or particles may be used in detecting,
 CC preventing or treating HPV infections and associated symptoms like
 CC dysplasia. The present sequence represents an HPV-16 LI codon optimised
 CC nucleotide sequence, which is given in the exemplification of the present
 CC invention.

XX Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 24; DB 9; Length 1515;

XX Best Local Similarity 100.0%; Pred. No. 1.3;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 669 ACCTCTCCACCTCCACCCGCC 692

DB 1471 ACCTCTCCACCTCCACCCGCC 1494

RESULT 14

ID AAD58571 standard; DNA; 1515 BP.

AC AAD58571;

DT 04-DEC-2003 (first entry)

DE HPV-16 LI codon optimised DNA.

XX Vaccine; humoral immunity; cell-mediated immunity; gene therapy; HPV;
 KW virucide; papillomavirus infection; gene; Human papillomavirus; ds.

XX Human papillomavirus.

Key Location/Qualifiers

FT CDS

FT 1..1515

FT /*tag= a

FT /product= "HPV-16 LI protein"

FT /transl_except= (pos:208..210,aa:Tyr)

FT /transl_except= (pos:295..297,aa:Val)

FT /note= "No stop codon"

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SUMMARIES

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5	1944	100.0	13	US-10-086-464-9	Sequence 9, Appl1
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18	1515	15	US-10-367-095-1	Sequence 1, Appl1
19	1515	16	US-10-368-046-1	Sequence 1, Appl1
20	1515	17	US-10-367-367-1	Sequence 1, Appl1
21	180	15	US-10-029-386-26494	Sequence 26494, A
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24	897	16	US-10-106-938A-11	Sequence 10, Appl1
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28	1289	15	US-10-106-938A-11	Sequence 59942, A
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32	4517	15	US-10-093-463-117	Sequence 1707, Ap
33	4586	10	US-09-983-000A-11	Sequence 4, Appl1
34	4586	15	US-10-102-524-1707	Sequence 11, Appl1
35	4586	17	US-10-304-019-4	Sequence 12, Appl1
36	4620	16	US-10-106-938A-11	Sequence 32, App
37	4620	17	US-10-304-019-11	Sequence 32, App
38	4620	17	US-10-648-593-52	Sequence 12, Appl1
39	4626	17	US-10-620-052A-11	Sequence 11, Appl1
40	4726	13	US-10-087-192-322	Sequence 52, Appl1
41	126974	17	US-10-304-019-12	Sequence 32, App
42	144035	13	US-10-087-192-322	Sequence 12, Appl1
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70	687	18	US-10-425-115-4643	Sequence 4643, Ap
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77	838	17	US-10-767-701-10055	Sequence 35074, A
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82	990	20	US-10-077-584-5	Sequence 5, Appl1
83	1002	14	US-10-437-963-72732	Sequence 72732, A
84	1101	17	US-10-424-599-59138	Sequence 59138, A
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92	20	1.0	1602	17	US-10-437-963-86675	Sequence 86675, A	165	19	1.0	358	15	US-10-212-679-168	Sequence 168, App
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95	20	1.0	1701	10	US-09-814-353-19123	Sequence 10, Appl	168	19	1.0	410	18	US-10-425-115-62860	Sequence 62860, A
96	20	1.0	1902	13	US-10-086-464-10	Sequence 61529, A	169	19	1.0	411	17	US-10-437-963-71834	Sequence 71834, A
97	20	1.0	1929	17	US-10-437-963-61529	Sequence 9, Appl	170	19	1.0	414	17	US-10-437-963-1558	Sequence 1558, Ap
98	20	1.0	1939	13	US-10-086-464-9	Sequence 2217, Ap	171	19	1.0	423	9	US-09-960-352-7506	Sequence 7506, Ap
99	20	1.0	1948	16	US-10-425-114-2217	Sequence 32612, Ap	172	19	1.0	430	17	US-10-437-963-100130	Sequence 100130, Ap
100	20	1.0	2120	16	US-10-425-114-35672	Sequence 53736, A	173	19	1.0	447	17	US-10-437-963-61225	Sequence 61225, A
101	20	1.0	2140	18	US-10-425-115-53736	Sequence 7, Appl	174	19	1.0	449	16	US-10-424-599-108799	Sequence 108799, A
102	20	1.0	2184	15	US-10-304-946-7	Sequence 726, App	175	19	1.0	455	17	US-10-767-701-29553	Sequence 29553, A
103	20	1.0	2185	18	US-10-739-930-726	Sequence 5, Appl	176	19	1.0	458	17	US-10-437-963-3398	Sequence 3398, Ap
104	20	1.0	2227	15	US-10-304-946-5	Sequence 6, Appl	177	19	1.0	459	17	US-10-437-963-34800	Sequence 34800, A
105	20	1.0	2242	15	US-10-304-946-6	Sequence 69331, A	178	19	1.0	460	17	US-10-437-963-49338	Sequence 49338, A
106	20	1.0	2250	17	US-10-437-963-69331	Sequence 8, Appl	179	19	1.0	463	9	US-09-864-761-5509	Sequence 5509, Ap
107	20	1.0	2411	15	US-10-304-946-8	Sequence 101060, A	180	19	1.0	465	10	US-09-918-995-25442	Sequence 25442, A
108	20	1.0	2443	17	US-10-437-963-101060	Sequence 101060, A	181	19	1.0	484	17	US-10-437-963-57511	Sequence 57511, A
109	20	1.0	2499	17	US-10-437-963-788	Sequence 788, App	182	19	1.0	486	16	US-10-424-599-11507	Sequence 11507, A
110	20	1.0	2553	17	US-10-437-963-69293	Sequence 69293, A	183	19	1.0	494	16	US-09-918-995-23336	Sequence 23336, A
111	20	1.0	2607	17	US-10-437-963-69298	Sequence 69298, A	184	19	1.0	495	16	US-10-424-599-11402	Sequence 11402, A
112	20	1.0	2621	15	US-10-128-714-159	Sequence 159, App	185	19	1.0	510	18	US-10-425-115-52035	Sequence 52035, A
113	20	1.0	2621	15	US-10-128-714-519	Sequence 5159, Ap	186	19	1.0	511	16	US-10-424-599-94642	Sequence 94642, A
114	20	1.0	2655	17	US-10-437-963-69336	Sequence 69336, A	187	19	1.0	531	9	US-09-864-761-22281	Sequence 22281, A
115	20	1.0	2853	17	US-10-437-963-69296	Sequence 69296, A	188	19	1.0	533	15	US-10-029-386-12535	Sequence 12535, Ap
116	20	1.0	2880	16	US-10-425-114-33031	Sequence 33031, A	189	19	1.0	563	13	US-10-027-632-5065	Sequence 5065, Ap
117	20	1.0	2881	16	US-10-425-114-33031	Sequence 33031, A	190	19	1.0	565	13	US-10-027-632-5066	Sequence 5066, Ap
118	20	1.0	2930	18	US-10-425-115-28209	Sequence 28209, A	191	19	1.0	565	13	US-10-027-632-5067	Sequence 5067, Ap
119	20	1.0	3046	15	US-10-437-963-69291	Sequence 69291, A	192	19	1.0	565	15	US-10-027-632-5066	Sequence 5066, Ap
120	20	1.0	3047	15	US-10-104-047-1149	Sequence 1149, Ap	193	19	1.0	565	15	US-10-027-632-5066	Sequence 5067, Ap
121	20	1.0	3097	14	US-10-101-664A-11	Sequence 11, Appl	194	19	1.0	565	15	US-10-027-632-5067	Sequence 664, App
122	20	1.0	3324	17	US-10-437-963-69380	Sequence 69380, A	195	19	1.0	575	13	US-10-029-386-62889	Sequence 32889, Ap
123	20	1.0	4017	17	US-10-437-963-56219	Sequence 56219, A	196	19	1.0	586	13	US-10-027-632-32290	Sequence 32290, Ap
124	20	1.0	4080	17	US-10-437-963-69380	Sequence 69380, A	197	19	1.0	586	13	US-10-027-632-32289	Sequence 32289, Ap
125	20	1.0	4248	17	US-10-437-963-88502	Sequence 88502, A	198	19	1.0	586	15	US-10-027-632-32289	Sequence 32289, Ap
126	20	1.0	4347	17	US-10-437-963-69382	Sequence 69382, A	199	19	1.0	597	18	US-10-425-115-50263	Sequence 50263, A
127	20	1.0	4644	17	US-10-437-963-85119	Sequence 85119, A	200	19	1.0	606	18	US-10-425-115-25320	Sequence 25320, A
128	20	1.0	4674	17	US-10-437-963-69259	Sequence 69259, A	201	19	1.0	626	17	US-10-767-701-26059	Sequence 26059, A
129	20	1.0	4883	17	US-10-437-963-92608	Sequence 92608, A	202	19	1.0	629	17	US-10-767-701-26059	Sequence 26059, A
130	20	1.0	4934	17	US-10-437-963-4830	Sequence 4830, Ap	203	19	1.0	635	16	US-10-260-238-1578	Sequence 1578, Ap
131	20	1.0	4960	17	US-10-437-963-85122	Sequence 85122, A	204	19	1.0	638	17	US-10-767-701-5619	Sequence 5619, Ap
132	20	1.0	5145	17	US-10-437-963-3509	Sequence 3509, Ap	205	19	1.0	643	16	US-10-425-114-18092	Sequence 18092, A
133	20	1.0	5157	9	US-09-764-877-2605	Sequence 2605, Ap	206	19	1.0	650	9	US-09-770-149-530	Sequence 530, App
134	20	1.0	5157	16	US-10-242-515-2605	Sequence 2605, Ap	207	19	1.0	650	16	US-10-424-599-123917	Sequence 123917, A
135	20	1.0	5199	16	US-09-764-877-2607	Sequence 2607, Ap	208	19	1.0	659	13	US-10-027-632-26916	Sequence 26916, A
136	20	1.0	5284	17	US-10-437-963-93167	Sequence 93167, A	209	19	1.0	682	13	US-10-027-632-26916	Sequence 26916, A
137	20	1.0	5720	9	US-09-800-729-18	Sequence 18, Appl	210	19	1.0	682	15	US-10-027-632-26915	Sequence 26915, A
138	20	1.0	5738	17	US-10-437-963-93221	Sequence 93221, A	211	19	1.0	682	15	US-10-027-632-26915	Sequence 26915, A
139	20	1.0	5769	17	US-09-764-853-134	Sequence 134, App	212	19	1.0	694	16	US-10-424-599-106215	Sequence 106215, A
140	20	1.0	5823	17	US-10-437-963-69258	Sequence 69258, A	213	19	1.0	704	16	US-10-425-114-14276	Sequence 14276, A
141	20	1.0	5868	15	US-10-293-504-2	Sequence 2, Appl	214	19	1.0	719	13	US-10-027-632-44208	Sequence 44208, A
142	20	1.0	6052	17	US-10-437-963-86097	Sequence 86097, A	215	19	1.0	728	13	US-10-027-632-44208	Sequence 44208, A
143	20	1.0	6135	17	US-10-437-963-14011	Sequence 14011, A	216	19	1.0	728	13	US-10-027-632-44208	Sequence 44208, A
144	20	1.0	6182	18	US-10-425-115-61630	Sequence 61630, A	217	19	1.0	728	13	US-10-027-632-44208	Sequence 44208, A
145	20	1.0	6402	17	US-10-437-963-16557	Sequence 16557, A	218	19	1.0	728	15	US-10-027-632-44208	Sequence 44208, A
146	20	1.0	6916	15	US-10-293-504-1	Sequence 1, Appl	219	19	1.0	743	18	US-10-027-632-44209	Sequence 44209, A
147	20	1.0	6972	17	US-10-437-963-16522	Sequence 16522, A	220	19	1.0	757	13	US-10-425-115-148725	Sequence 148725, A
148	20	1.0	7142	16	US-10-467-042-21	Sequence 21, Appl	221	19	1.0	757	13	US-10-027-632-19434	Sequence 19434, A
149	20	1.0	7142	16	US-10-467-042-21	Sequence 21, Appl	222	19	1.0	757	13	US-10-027-632-19434	Sequence 19434, A
150	20	1.0	41100	9	US-09-755-665-46	Sequence 46, Appl	223	19	1.0	757	13	US-10-027-632-19434	Sequence 19434, A
151	20	1.0	41100	9	US-10-629-248-46	Sequence 46, Appl	224	19	1.0	817	18	US-10-425-114-83110	Sequence 83110, A
152	20	1.0	87394	18	US-10-810-788A-6	Sequence 6, Appl	225	19	1.0	830	16	US-10-425-115-8518	Sequence 8518, Ap
153	20	1.0	109453	17	US-10-388-838-81	Sequence 81, Appl	226	19	1.0	836	17	US-10-437-963-64836	Sequence 64836, A
154	20	1.0	9025608	15	US-10-156-761-1	Sequence 1, Appl	227	19	1.0	836	17	US-10-425-115-8525	Sequence 8525, Ap
155	19	1.0	105	15	US-10-023-386-14368	Sequence 14368, A	228	19	1.0	836	17	US-10-437-963-64836	Sequence 64836, A
156	19	1.0	141	15	US-10-023-386-15226	Sequence 15226, A	229	19	1.0	853	17	US-10-767-701-2738	Sequence 2738, Ap
157	19	1.0	217	18	US-10-425-115-102419	Sequence 102419, A	230	19	1.0	889	17	US-10-437-963-66233	Sequence 66233, A
158	19	1.0	257	18	US-10-425-115-47774	Sequence 47774, A	231	19	1.0	909	15	US-10-076-747-10	Sequence 10, Appl

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C 233	19	1.0	925	16	US-10-422-114-33081	Sequence 33081, A	C 306	19	1.0	8811	15	US-10-120-801-25	Sequence 25, App
C 234	19	1.0	925	18	US-10-422-115-83113	Sequence 83113, A	C 307	19	1.0	9487	18	US-10-788-792-43	Sequence 43, App
C 235	19	1.0	998	18	US-10-425-115-18367	Sequence 18367, A	C 308	19	1.0	9567	10	US-09-738-630-58	Sequence 58, App
C 236	19	1.0	1023	17	US-10-437-963-59357	Sequence 59357, A	C 309	19	1.0	9667	13	US-10-016-768-12	Sequence 12, App
C 237	19	1.0	1029	17	US-10-437-963-95316	Sequence 95316, A	C 310	19	1.0	9674	13	US-10-016-768-9	Sequence 9, App
C 238	19	1.0	1056	16	US-10-425-114-23357	Sequence 23357, A	C 311	19	1.0	9574	13	US-10-016-768-9	Sequence 494, App
C 239	19	1.0	1062	18	US-10-425-115-8520	Sequence 8520, App	C 312	19	1.0	16750	15	US-10-311-455-494	Sequence 36, App
C 240	19	1.0	1074	16	US-10-424-599-41696	Sequence 41696, A	C 313	19	1.0	16750	16	US-10-221-714A-36	Sequence 1048, App
C 241	19	1.0	1074	18	US-10-425-115-12663	Sequence 12663, A	C 314	19	1.0	27406	13	US-10-087-192-1048	Sequence 1933, App
C 242	19	1.0	1077	16	US-10-425-114-33789	Sequence 33789, A	C 315	19	1.0	31124	13	US-10-087-192-1393	Sequence 463, App
C 243	19	1.0	1185	18	US-10-425-114-33789	Sequence 33789, A	C 316	19	1.0	60452	13	US-10-087-192-1900	Sequence 1900, App
C 244	19	1.0	1185	18	US-10-425-115-8522	Sequence 8522, App	C 317	19	1.0	75976	17	US-10-322-281-229	Sequence 229, App
C 245	19	1.0	1297	18	US-10-739-930-5335	Sequence 5335, App	C 318	19	1.0	174448	13	US-10-087-192-148	Sequence 148, App
C 246	19	1.0	1297	17	US-10-437-963-96339	Sequence 96339, A	C 319	19	1.0	246940	17	US-10-332-696-58	Sequence 58, App
C 247	19	1.0	1293	17	US-10-437-963-50650	Sequence 50650, A	C 320	19	1.0	430442	18	US-10-417-375-128	Sequence 128, App
C 248	19	1.0	1293	17	US-10-437-963-39781	Sequence 39781, A	C 321	19	1.0	659158	9	US-09-771-208-20	Sequence 20, App
C 249	19	1.0	1309	17	US-10-437-963-40685	Sequence 40685, A	C 322	19	1.0	18	13	US-10-086-464-25	Sequence 25, App
C 250	19	1.0	1322	17	US-10-437-963-12388	Sequence 12388, A	C 323	19	1.0	145	9	US-10-481-763-47	Sequence 27, App
C 251	19	1.0	1365	17	US-10-767-701-15550	Sequence 15550, A	C 324	19	0.9	145	9	US-09-867-701-8952	Sequence 8952, App
C 252	19	1.0	1380	18	US-10-739-930-577	Sequence 577, App	C 325	19	0.9	147	18	US-10-674-124A-14669	Sequence 14669, A
C 253	19	1.0	1460	17	US-10-437-963-39454	Sequence 39454, A	C 326	19	0.9	162	17	US-10-674-124A-14669	Sequence 19520, A
C 254	19	1.0	1461	18	US-10-425-115-101777	Sequence 101777, A	C 327	19	0.9	195	9	US-09-867-701-8949	Sequence 8949, App
C 255	19	1.0	1545	17	US-10-437-963-86830	Sequence 86830, A	C 328	19	0.9	195	9	US-10-425-115-111603	Sequence 111603, A
C 256	19	1.0	1546	17	US-10-437-963-9218	Sequence 9218, App	C 329	19	0.9	201	9	US-09-867-701-8773	Sequence 8773, App
C 257	19	1.0	1652	15	US-10-369-493-27227	Sequence 27227, A	C 330	19	0.9	203	9	US-09-738-973-480	Sequence 480, App
C 258	19	1.0	1661	17	US-10-437-963-59005	Sequence 59005, A	C 331	19	0.9	203	9	US-09-867-701-9051	Sequence 9051, App
C 259	19	1.0	1715	17	US-10-437-963-87635	Sequence 87635, A	C 332	19	0.9	203	9	US-09-854-133-480	Sequence 480, App
C 260	19	1.0	1971	18	US-10-425-115-133331	Sequence 133331, A	C 333	19	0.9	203	15	US-10-114-649A-480	Sequence 480, App
C 261	19	1.0	2025	13	US-10-086-464-103	Sequence 13, App	C 334	19	0.9	203	18	US-10-674-124A-5687	Sequence 5687, App
C 262	19	1.0	2095	16	US-10-425-114-30026	Sequence 30026, A	C 335	19	0.9	209	9	US-09-867-701-8665	Sequence 8665, App
C 263	19	1.0	2104	13	US-10-086-464-12	Sequence 12, App	C 336	19	0.9	216	18	US-10-674-124A-22637	Sequence 20309, A
C 264	19	1.0	2107	16	US-10-424-599-129942	Sequence 129942, A	C 337	19	0.9	227	17	US-09-864-761-19728	Sequence 19728, A
C 265	19	1.0	2191	17	US-10-437-963-6429	Sequence 6429, App	C 338	19	0.9	227	18	US-10-437-963-13373	Sequence 13373, A
C 266	19	1.0	2247	17	US-10-437-963-73541	Sequence 73541, A	C 339	19	0.9	234	17	US-10-437-963-1179	Sequence 1179, A
C 267	19	1.0	2256	17	US-10-437-963-16256	Sequence 16256, A	C 340	19	0.9	247	17	US-10-437-963-1179	Sequence 4179, App
C 268	19	1.0	2327	17	US-10-437-963-4440	Sequence 4440, A	C 341	19	0.9	247	17	US-10-437-963-12038	Sequence 72038, A
C 269	19	1.0	2421	16	US-10-623-272-4	Sequence 5440, A	C 342	19	0.9	251	17	US-10-437-963-99520	Sequence 99520, A
C 270	19	1.0	2487	16	US-10-623-272-54	Sequence 5440, A	C 343	19	0.9	262	17	US-10-437-963-88261	Sequence 88261, A
C 271	19	1.0	2603	15	US-10-094-749-753	Sequence 753, App	C 344	19	0.9	262	18	US-09-867-701-8858	Sequence 8858, App
C 272	19	1.0	2699	17	US-10-437-963-1877	Sequence 1877, App	C 345	19	0.9	266	18	US-10-425-115-143302	Sequence 143302, A
C 273	19	1.0	2850	17	US-10-437-963-5398	Sequence 5398, App	C 346	19	0.9	272	17	US-09-867-701-8694	Sequence 8694, App
C 274	19	1.0	2982	17	US-10-437-963-30948	Sequence 30948, A	C 347	19	0.9	272	17	US-10-437-963-11513	Sequence 11513, A
C 275	19	1.0	3096	17	US-10-437-963-5387	Sequence 5387, App	C 348	19	0.9	274	10	US-09-923-876-5151	Sequence 5151, App
C 276	19	1.0	3517	15	US-10-104-047-102	Sequence 102, App	C 349	19	0.9	278	9	US-09-974-300-6480	Sequence 6480, App
C 277	19	1.0	3600	15	US-10-023-888-1	Sequence 1, App	C 350	19	0.9	284	9	US-09-294-033B-1608	Sequence 1608, App
C 278	19	1.0	3600	15	US-10-023-889-1	Sequence 1, App	C 351	19	0.9	297	9	US-09-294-033B-3921	Sequence 3921, App
C 279	19	1.0	3600	15	US-10-023-890-1	Sequence 1, App	C 352	19	0.9	300	9	US-09-294-033B-1720	Sequence 1720, App
C 280	19	1.0	3600	15	US-10-024-197-1	Sequence 1, App	C 353	19	0.9	303	9	US-09-816-279-3	Sequence 3, App
C 281	19	1.0	3600	15	US-10-023-894-1	Sequence 1, App	C 354	19	0.9	319	17	US-10-437-963-21372	Sequence 21372, A
C 282	19	1.0	3621	9	US-09-895-072-21	Sequence 21, App	C 355	19	0.9	321	9	US-09-933-797-351	Sequence 351, App
C 283	19	1.0	3621	9	US-09-895-072-21	Sequence 21, App	C 356	19	0.9	321	18	US-10-674-124A-7446	Sequence 7446, App
C 284	19	1.0	3621	15	US-10-306-686-21	Sequence 21, App	C 357	19	0.9	340	16	US-10-424-599-42777	Sequence 42777, A
C 285	19	1.0	3783	9	US-09-895-072-20	Sequence 20, App	C 358	19	0.9	340	16	US-10-424-599-42777	Sequence 42777, A
C 286	19	1.0	3783	9	US-09-895-072-20	Sequence 20, App	C 359	19	0.9	340	16	US-10-424-599-42777	Sequence 42777, A
C 287	19	1.0	3783	15	US-10-306-686-20	Sequence 20, App	C 360	19	0.9	357	11	US-09-864-761-7797	Sequence 7797, App
C 288	19	1.0	4373	17	US-10-306-686-20	Sequence 20, App	C 361	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
C 289	19	1.0	4413	16	US-10-424-599-141147	Sequence 141147, A	C 362	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
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C 291	19	1.0	4842	17	US-10-437-963-5193	Sequence 5193, App	C 364	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
C 292	19	1.0	5252	15	US-10-172-118-35	Sequence 35, App	C 365	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
C 293	19	1.0	5252	16	US-10-342-887-35	Sequence 35, App	C 366	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
C 294	19	1.0	5597	9	US-09-895-072-4	Sequence 4, App	C 367	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
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C 296	19	1.0	5597	15	US-10-023-888-3	Sequence 3, App	C 369	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
C 297	19	1.0	5597	15	US-10-023-889-3	Sequence 3, App	C 370	19	0.9	361	16	US-09-864-761-7797	Sequence 7797, App
C 298	19	1.0	5597	15	US-10-023-890-3	Sequence 3, App	C 371	19	0.9	362	16	US-10-091-504-1325	Sequence 1325, App
C 299	19	1.0	5597	15	US-10-024-197-3	Sequence 3, App	C 372	19	0.9	362	16	US-10-091-504-1325	Sequence 1325, App
C 300	19	1.0	5597	15	US-10-023-894-3	Sequence 3, App	C 373	19	0.9	367	11	US-09-732-627A-1118	Sequence 1118, App
C 301	19	1.0	5597	15	US-10-306-86-4	Sequence 4, App	C 374	19	0.9	375	11	US-09-864-761-17485	Sequence 17485, A
C 302	19	1.0	5810	17	US-10-437-963-54024	Sequence 54024, A	C 375	19	0.9	378	11	US-09-732-627A-1464	Sequence 1464, App
C 303	19	1.0	6616	15	US-10-311-455-448	Sequence 448, App	C 376	19	0.9	382	10	US-09-803-719-9	Sequence 9, App
C 304	19	1.0	6754	16	US-10-221-613-265	Sequence 265, App	C 377	19	0.9	386	11	US-09-732-627A-3915	Sequence 3915, App

C 378	18	0.9	386	18	US-10-674-124A-23154	Sequence 23154, A
C 379	18	0.9	390	17	US-10-437-963-73339	Sequence 73339, A
C 380	18	0.9	396	17	US-10-437-963-40111	Sequence 40111, A
C 381	18	0.9	421	18	US-10-425-115-158331	Sequence 158331, A
C 382	18	0.9	430	13	US-10-027-632-83597	Sequence 83597, A
C 383	18	0.9	430	13	US-10-027-632-316141	Sequence 316141, A
C 384	18	0.9	430	15	US-10-027-632-83597	Sequence 83597, A
C 385	18	0.9	430	15	US-10-027-632-316141	Sequence 316141, A
C 386	18	0.9	430	18	US-10-674-124A-9824	Sequence 9824, Ap
C 387	18	0.9	438	16	US-10-424-599-27753	Sequence 27753, A
C 388	18	0.9	438	18	US-10-674-124A-21659	Sequence 21659, A
C 389	18	0.9	439	9	US-09-876-889-273	Sequence 273, App
C 390	18	0.9	441	13	US-10-027-632-41035	Sequence 41035, A
C 391	18	0.9	441	15	US-10-027-632-41035	Sequence 41035, A
C 392	18	0.9	443	16	US-10-424-599-16042	Sequence 16042, A
C 393	18	0.9	443	17	US-10-437-963-102112	Sequence 102112, A
C 394	18	0.9	450	9	US-09-864-761-11696	Sequence 11696, A
C 395	18	0.9	452	17	US-10-437-963-74371	Sequence 74371, A
C 396	18	0.9	452	18	US-10-674-124A-4960	Sequence 4960, Ap
C 397	18	0.9	462	16	US-10-424-599-23031	Sequence 23031, A
C 398	18	0.9	465	9	US-09-864-761-23120	Sequence 23120, A
C 399	18	0.9	470	9	US-09-864-761-2442	Sequence 2442, Ap
C 400	18	0.9	474	9	US-09-864-761-1685	Sequence 1685, Ap
C 401	18	0.9	474	9	US-09-864-761-3616	Sequence 3616, Ap
C 402	18	0.9	475	18	US-10-674-124A-17053	Sequence 17053, A
C 403	18	0.9	477	9	US-09-864-761-698	Sequence 698, App
C 404	18	0.9	477	9	US-09-864-761-5954	Sequence 5954, Ap
C 405	18	0.9	479	9	US-09-864-761-3539	Sequence 3539, Ap
C 406	18	0.9	481	17	US-10-767-701-25413	Sequence 25413, A
C 407	18	0.9	486	9	US-09-864-761-6405	Sequence 6405, Ap
C 408	18	0.9	491	16	US-10-424-599-76655	Sequence 76655, A
C 409	18	0.9	491	18	US-10-425-115-39559	Sequence 39559, A
C 410	18	0.9	493	17	US-10-021-323-9316	Sequence 9316, Ap
C 411	18	0.9	494	9	US-09-864-761-2947	Sequence 2947, Ap
C 412	18	0.9	495	18	US-10-425-115-65791	Sequence 65791, A
C 413	18	0.9	496	9	US-09-864-761-10689	Sequence 10689, A
C 414	18	0.9	499	13	US-10-027-632-136133	Sequence 136133, A
C 415	18	0.9	499	15	US-10-027-632-136133	Sequence 136133, A
C 416	18	0.9	502	17	US-10-437-963-26384	Sequence 26384, A
C 417	18	0.9	504	17	US-10-437-963-24614	Sequence 24614, A
C 418	18	0.9	511	9	US-09-864-761-18441	Sequence 18441, A
C 419	18	0.9	511	9	US-09-864-761-20384	Sequence 20384, A
C 420	18	0.9	517	16	US-10-424-599-106345	Sequence 106345, A
C 421	18	0.9	521	9	US-09-917-800A-1194	Sequence 1194, Ap
C 422	18	0.9	529	17	US-10-767-701-915	Sequence 915, App
C 423	18	0.9	532	17	US-10-425-114-3128	Sequence 3128, Ap
C 424	18	0.9	532	17	US-10-767-701-27386	Sequence 27386, A
C 425	18	0.9	533	17	US-10-437-963-9878	Sequence 9878, Ap
C 426	18	0.9	545	13	US-10-027-632-238238	Sequence 238238, A
C 427	18	0.9	545	15	US-10-027-632-238238	Sequence 238238, A
C 428	18	0.9	545	16	US-10-424-599-79534	Sequence 79534, A
C 429	18	0.9	560	13	US-10-027-632-260145	Sequence 260145, A
C 430	18	0.9	560	13	US-10-027-632-260146	Sequence 260146, A
C 431	18	0.9	560	15	US-10-027-632-260145	Sequence 260145, A
C 432	18	0.9	560	16	US-10-027-632-260146	Sequence 260146, A
C 433	18	0.9	560	15	US-10-425-114-27621	Sequence 27621, A
C 434	18	0.9	563	17	US-10-021-323-15398	Sequence 15398, A
C 435	18	0.9	564	17	US-10-021-323-15398	Sequence 15398, A
C 436	18	0.9	573	18	US-10-425-115-43899	Sequence 43899, A
C 437	18	0.9	582	17	US-10-767-701-1988	Sequence 1988, Ap
C 438	18	0.9	586	15	US-10-029-386-1030	Sequence 1030, Ap
C 439	18	0.9	591	17	US-10-021-323-1656	Sequence 1656, Ap
C 440	18	0.9	594	16	US-10-425-114-1806	Sequence 1806, Ap
C 441	18	0.9	596	13	US-10-027-632-270692	Sequence 270692, A
C 442	18	0.9	596	15	US-10-027-632-270692	Sequence 270692, A
C 443	18	0.9	598	15	US-10-029-386-3466	Sequence 3466, Ap
C 444	18	0.9	613	17	US-10-767-701-24505	Sequence 24505, A
C 445	18	0.9	614	13	US-10-027-632-3982	Sequence 3982, Ap
C 446	18	0.9	614	15	US-10-027-632-3982	Sequence 3982, Ap
C 447	18	0.9	629	15	US-10-425-115-148410	Sequence 148410, A
C 448	18	0.9	632	13	US-10-027-632-228421	Sequence 228421, A
C 449	18	0.9	632	15	US-10-027-632-228421	Sequence 228421, A
C 450	18	0.9	633	16	US-10-425-114-1974	Sequence 1974, Ap
C 451	18	0.9	636	17	US-10-767-701-25393	Sequence 25393, A
C 452	18	0.9	637	17	US-10-767-701-13942	Sequence 13942, A
C 453	18	0.9	640	16	US-10-424-599-3769	Sequence 3769, A
C 454	18	0.9	642	17	US-10-021-323-8680	Sequence 8680, Ap
C 455	18	0.9	643	17	US-10-767-701-9329	Sequence 9329, Ap
C 456	18	0.9	644	17	US-10-767-701-26613	Sequence 26613, A
C 457	18	0.9	648	17	US-10-767-701-26061	Sequence 26061, A
C 458	18	0.9	657	9	US-09-833-381-921	Sequence 921, App
C 459	18	0.9	658	16	US-10-425-114-20639	Sequence 20639, A
C 460	18	0.9	659	17	US-10-767-701-12351	Sequence 12351, A
C 461	18	0.9	662	13	US-10-027-632-172453	Sequence 172453, A
C 462	18	0.9	662	15	US-10-027-632-172453	Sequence 172453, A
C 463	18	0.9	674	10	US-09-919-039-261	Sequence 261, App
C 464	18	0.9	676	13	US-10-027-632-234699	Sequence 234699, A
C 465	18	0.9	676	15	US-10-027-632-234699	Sequence 234699, A
C 466	18	0.9	676	15	US-10-027-632-234700	Sequence 234700, A
C 467	18	0.9	678	16	US-10-425-114-30644	Sequence 30644, A
C 468	18	0.9	683	18	US-10-425-115-43821	Sequence 43821, A
C 469	18	0.9	683	18	US-10-425-115-52891	Sequence 52891, A
C 470	18	0.9	691	14	US-10-198-846-11852	Sequence 11852, A
C 471	18	0.9	697	18	US-10-425-115-94860	Sequence 94860, A
C 472	18	0.9	704	17	US-10-767-701-5945	Sequence 5945, Ap
C 473	18	0.9	708	13	US-10-027-632-28298	Sequence 28298, A
C 474	18	0.9	708	15	US-10-425-115-163175	Sequence 163175, A
C 475	18	0.9	719	18	US-10-425-115-126748	Sequence 126748, A
C 476	18	0.9	721	18	US-10-424-599-109452	Sequence 109452, A
C 477	18	0.9	729	16	US-10-424-599-4027	Sequence 4027, Ap
C 478	18	0.9	734	16	US-10-424-599-4027	Sequence 4027, Ap
C 479	18	0.9	742	18	US-10-425-115-125730	Sequence 125730, A
C 480	18	0.9	746	9	US-09-910-943-885	Sequence 943, App
C 481	18	0.9	746	17	US-10-767-701-13193	Sequence 13193, A
C 482	18	0.9	747	17	US-10-437-963-50399	Sequence 50399, A
C 483	18	0.9	760	18	US-10-425-115-29176	Sequence 29176, A
C 484	18	0.9	769	18	US-10-739-930-4340	Sequence 4340, Ap
C 485	18	0.9	775	17	US-10-437-963-90950	Sequence 90950, A
C 486	18	0.9	777	18	US-10-425-115-80497	Sequence 80497, A
C 487	18	0.9	777	18	US-10-424-599-13897	Sequence 13897, A
C 488	18	0.9	794	16	US-10-027-632-8651	Sequence 8651, Ap
C 489	18	0.9	794	13	US-10-027-632-8652	Sequence 8652, Ap
C 490	18	0.9	794	15	US-10-027-632-8651	Sequence 8651, Ap
C 491	18	0.9	794	15	US-10-027-632-8652	Sequence 8652, Ap
C 492	18	0.9	794	15	US-10-259-165-429	Sequence 429, App
C 493	18	0.9	801	15	US-10-425-114-8763	Sequence 8763, Ap
C 494	18	0.9	809	16	US-10-437-963-78950	Sequence 78950, A
C 495	18	0.9	814	17	US-10-437-963-73949	Sequence 73949, A
C 496	18	0.9	825	17	US-10-437-963-99757	Sequence 99757, A
C 497	18	0.9	825	17	US-10-437-963-99757	Sequence 99757, A
C 498	18	0.9	832	17	US-10-767-701-11455	Sequence 11455, A
C 499	18	0.9	839	9	US-09-974-300-6508	Sequence 6508, Ap
C 500	18	0.9	839	9	US-09-974-300-6528	Sequence 6528, Ap
C 501	18	0.9	839	9	US-10-425-115-132071	Sequence 132071, A
C 502	18	0.9	849	14	US-10-198-846-1519	Sequence 3519, Ap
C 503	18	0.9	849	14	US-10-198-846-1519	Sequence 3519, Ap
C 504	18	0.9	851	16	US-10-425-115-53800	Sequence 53800, A
C 505	18	0.9	851	16	US-10-424-599-14725	Sequence 14725, A
C 506	18	0.9	855	18	US-10-425-115-132419	Sequence 132419, A
C 507	18	0.9	861	9	US-09-938-842A-2206	Sequence 2206, Ap
C 508	18	0.9	861	11	US-09-938-842A-2206	Sequence 2206, Ap
C 509	18	0.9	863	13	US-10-027-632-156867	Sequence 156867, A
C 510	18	0.9	863	13	US-10-027-632-156867	Sequence 156867, A
C 511	18	0.9	863	13	US-10-027-632-156867	Sequence 156867, A
C 512	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 513	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 514	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 515	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 516	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 517	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 518	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 519	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 520	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 521	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 522	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 523	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A

C 524	18	0.9	904	18	US-10-425-115-23909	Sequence 23909, A
C 525	18	0.9	910	9	US-09-880-107-1602	Sequence 1602, Ap
526	18	0.9	910	13	US-10-027-632-162147	Sequence 162147, A
527	18	0.9	910	15	US-10-027-632-162147	Sequence 162147, A
528	18	0.9	936	18	US-10-425-115-5837	Sequence 5837, Ap
C 529	18	0.9	956	17	US-10-437-963-19506	Sequence 19506, A
C 530	18	0.9	957	18	US-10-739-930-2223	Sequence 2223, Ap
C 531	18	0.9	960	17	US-10-437-963-60424	Sequence 60424, A
C 532	18	0.9	963	17	US-10-437-963-82835	Sequence 82835, A
C 533	18	0.9	972	16	US-10-424-599-14296	Sequence 14296, A
C 534	18	0.9	1008	16	US-10-464-610-1	Sequence 1, Appl
C 535	18	0.9	1004	16	US-10-320-797-2131	Sequence 2131, Ap
C 536	18	0.9	1030	18	US-10-425-115-25644	Sequence 25644, A
C 537	18	0.9	1036	16	US-10-424-599-32223	Sequence 32223, A
C 538	18	0.9	1048	15	US-10-369-493-27877	Sequence 27877, A
C 539	18	0.9	1058	18	US-10-425-115-73539	Sequence 73539, A
C 540	18	0.9	1060	18	US-10-425-115-128138	Sequence 128138, A
C 541	18	0.9	1110	15	US-10-411-224-11	Sequence 11, Appl
C 542	18	0.9	1110	16	US-10-047-021-11	Sequence 11, Appl
C 543	18	0.9	1116	16	US-10-425-114-9652	Sequence 9652, Ap
C 544	18	0.9	1117	18	US-10-425-115-128136	Sequence 128136, A
C 545	18	0.9	1123	18	US-10-425-115-69967	Sequence 69967, A
C 546	18	0.9	1132	16	US-10-424-599-119632	Sequence 119632, A
C 547	18	0.9	1134	16	US-10-424-599-119632	Sequence 27834, A
C 548	18	0.9	1143	15	US-09-910-186A-27	Sequence 27, Appl
C 549	18	0.9	1149	13	US-10-027-632-10356	Sequence 10356, A
C 550	18	0.9	1149	13	US-10-027-632-10357	Sequence 10357, A
C 551	18	0.9	1149	13	US-10-027-632-10358	Sequence 10358, A
C 552	18	0.9	1149	13	US-10-027-632-10358	Sequence 10356, A
C 553	18	0.9	1149	15	US-10-027-632-10357	Sequence 10357, A
C 554	18	0.9	1149	15	US-10-027-632-10357	Sequence 10358, A
C 555	18	0.9	1149	15	US-10-027-632-10358	Sequence 8200, Ap
C 556	18	0.9	1174	17	US-10-767-701-8200	Sequence 8200, Ap
C 557	18	0.9	1181	16	US-10-415-134-3	Sequence 3, Appl
C 558	18	0.9	1218	16	US-10-425-114-27112	Sequence 27112, A
C 559	18	0.9	1219	18	US-10-425-115-58743	Sequence 58743, A
C 560	18	0.9	1224	17	US-10-437-963-11898	Sequence 11898, A
C 561	18	0.9	1232	18	US-10-425-115-157174	Sequence 157174, A
C 562	18	0.9	1246	17	US-10-437-963-56227	Sequence 56227, A
C 563	18	0.9	1267	17	US-10-767-701-10450	Sequence 10450, A
C 564	18	0.9	1272	17	US-10-767-701-14463	Sequence 14463, A
C 565	18	0.9	1273	16	US-10-425-114-35619	Sequence 35619, A
C 566	18	0.9	1273	17	US-10-437-963-44884	Sequence 44884, A
C 567	18	0.9	1275	17	US-10-437-963-49222	Sequence 49233, A
C 568	18	0.9	1286	17	US-10-437-963-49222	Sequence 45794, A
C 569	18	0.9	1295	16	US-10-282-122A-20115	Sequence 20115, A
C 570	18	0.9	1323	17	US-10-437-963-49235	Sequence 49235, A
C 571	18	0.9	1355	16	US-10-425-114-25775	Sequence 25775, A
C 572	18	0.9	1364	17	US-10-437-963-76875	Sequence 76875, A
C 573	18	0.9	1376	18	US-10-425-115-112979	Sequence 112979, A
C 574	18	0.9	1380	16	US-10-424-599-54926	Sequence 54926, A
C 575	18	0.9	1387	17	US-10-437-963-12714	Sequence 12714, A
C 576	18	0.9	1387	17	US-10-437-963-12714	Sequence 88707, A
C 577	18	0.9	1390	10	US-09-933-767-124	Sequence 124, App
C 578	18	0.9	1390	14	US-10-004-860-124	Sequence 124, App
C 579	18	0.9	1390	14	US-10-023-282-124	Sequence 124, App
C 580	18	0.9	1392	16	US-10-320-797-1131	Sequence 1131, Ap
C 581	18	0.9	1401	16	US-10-424-599-89804	Sequence 89804, A
C 582	18	0.9	1408	16	US-10-425-114-15596	Sequence 15596, A
C 583	18	0.9	1417	18	US-10-425-115-52892	Sequence 52892, A
C 584	18	0.9	1452	18	US-10-793-639-317	Sequence 317, App
C 585	18	0.9	1464	17	US-10-437-963-7077	Sequence 7077, Ap
C 586	18	0.9	1471	16	US-10-424-599-129382	Sequence 129382, A
C 587	18	0.9	1520	16	US-10-739-930-1666	Sequence 1666, Ap
C 588	18	0.9	1525	16	US-10-424-599-23293	Sequence 23293, A
C 589	18	0.9	1539	18	US-10-425-115-36325	Sequence 36325, A
C 590	18	0.9	1544	16	US-10-276-774-982	Sequence 982, App
C 591	18	0.9	1554	17	US-10-437-963-6874	Sequence 6874, Ap
C 592	18	0.9	1563	15	US-10-425-115-102018	Sequence 102018, A
C 593	18	0.9	1590	18	US-10-425-115-128137	Sequence 128137, A
C 594	18	0.9	1597	17	US-10-424-599-39222	Sequence 39222, A
C 595	18	0.9	1617	16	US-10-437-963-53894	Sequence 53894, A
C 596	18	0.9	1621	16	US-10-425-114-3084	Sequence 3084, Ap
C 597	18	0.9	1638	16	US-10-425-114-11638	Sequence 11638, A
598	18	0.9	1645	16	US-10-424-599-110728	Sequence 110728, A
599	18	0.9	1656	16	US-10-425-114-34761	Sequence 34761, A
600	18	0.9	1662	16	US-10-425-114-33883	Sequence 33883, A
601	18	0.9	1669	17	US-10-437-963-69399	Sequence 69399, A
C 602	18	0.9	1680	13	US-10-027-632-264413	Sequence 264413, A
C 603	18	0.9	1680	15	US-10-027-632-264413	Sequence 264413, A
C 604	18	0.9	1684	9	US-09-764-877-3818	Sequence 3818, Ap
C 605	18	0.9	1684	16	US-10-242-515-2818	Sequence 2818, Ap
C 606	18	0.9	1719	16	US-10-425-114-28183	Sequence 28183, A
C 607	18	0.9	1734	15	US-10-172-118-1726	Sequence 1726, Ap
C 608	18	0.9	1734	16	US-10-342-887-1726	Sequence 1726, Ap
C 609	18	0.9	1751	17	US-10-437-963-9763	Sequence 9763, Ap
C 610	18	0.9	1753	16	US-10-437-963-35008	Sequence 35008, A
C 611	18	0.9	1759	16	US-10-425-114-14300	Sequence 340, App
C 612	18	0.9	1769	18	US-10-425-115-65582	Sequence 65582, A
C 613	18	0.9	1774	18	US-10-425-115-147000	Sequence 147000, A
C 614	18	0.9	1777	18	US-10-425-115-122008	Sequence 122008, A
C 615	18	0.9	1787	18	US-10-425-115-81653	Sequence 81653, A
C 616	18	0.9	1799	17	US-10-437-963-20536	Sequence 20536, A
C 617	18	0.9	1806	18	US-10-425-115-178673	Sequence 178673, A
C 618	18	0.9	1840	11	US-09-973-278-921	Sequence 921, App
C 619	18	0.9	1846	17	US-10-437-963-92205	Sequence 92205, A
C 620	18	0.9	1849	17	US-10-437-963-92205	Sequence 92205, A
C 621	18	0.9	1862	18	US-10-425-115-147001	Sequence 147001, A
C 622	18	0.9	1878	11	US-09-938-842A-1413	Sequence 1413, Ap
C 623	18	0.9	1878	9	US-09-938-842A-1413	Sequence 1413, Ap
C 624	18	0.9	1895	16	US-10-424-599-117416	Sequence 117416, A
C 625	18	0.9	1910	13	US-10-027-632-99815	Sequence 99815, A
C 626	18	0.9	1910	13	US-10-027-632-99816	Sequence 99816, A
C 627	18	0.9	1910	13	US-10-027-632-99816	Sequence 99817, A
C 628	18	0.9	1910	15	US-10-027-632-99817	Sequence 99815, A
C 629	18	0.9	1910	15	US-10-027-632-99817	Sequence 99816, A
C 630	18	0.9	1910	15	US-10-027-632-99817	Sequence 99817, A
C 631	18	0.9	1925	15	US-10-369-493-35962	Sequence 35962, A
C 632	18	0.9	1933	17	US-10-437-963-6806	Sequence 6806, Ap
C 633	18	0.9	1935	16	US-10-424-599-1380802	Sequence 1380802, A
C 634	18	0.9	1941	17	US-10-437-963-5385	Sequence 5385, Ap
C 635	18	0.9	1962	9	US-09-938-842A-2542	Sequence 2542, Ap
C 636	18	0.9	1962	11	US-10-108-260A-129	Sequence 129, App
C 637	18	0.9	1969	16	US-09-938-842A-2542	Sequence 4, Appl
C 638	18	0.9	1986	15	US-10-242-568-4	Sequence 4, Appl
C 639	18	0.9	1986	16	US-10-425-114-15609	Sequence 15609, A
C 640	18	0.9	1986	15	US-10-425-114-15609	Sequence 174166, A
C 641	18	0.9	2000	11	US-09-938-842A-4104	Sequence 4104, Ap
C 642	18	0.9	2000	9	US-09-938-842A-4104	Sequence 4104, Ap
C 643	18	0.9	2007	16	US-10-425-114-3832	Sequence 3832, Ap
C 644	18	0.9	2038	9	US-09-880-107-1102	Sequence 1102, Ap
C 645	18	0.9	2056	17	US-10-437-963-72774	Sequence 72774, A
C 646	18	0.9	2061	17	US-10-437-963-71684	Sequence 71684, A
C 647	18	0.9	2065	16	US-10-437-963-71684	Sequence 35471, A
C 648	18	0.9	2065	16	US-10-425-114-35471	Sequence 16029, A
C 649	18	0.9	2067	15	US-10-310-154-54	Sequence 174166, A
C 650	18	0.9	2093	15	US-10-037-870-999	Sequence 999, App
C 651	18	0.9	2093	15	US-10-117-722-999	Sequence 1274, Ap
C 652	18	0.9	2102	15	US-10-104-047-1274	Sequence 101215, A
C 653	18	0.9	2119	17	US-10-437-963-101275	Sequence 11650, A
C 654	18	0.9	2122	18	US-10-425-115-118650	Sequence 118650, A
C 655	18	0.9	2132	17	US-10-767-701-13570	Sequence 13570, A
C 656	18	0.9	2145	17	US-10-437-963-12104	Sequence 12104, A
C 657	18	0.9	2152	16	US-10-424-599-90186	Sequence 90186, A
C 658	18	0.9	2157	17	US-10-437-963-38370	Sequence 38370, A
C 659	18	0.9	2187	17	US-10-437-963-6708	Sequence 6708, Ap
C 660	18	0.9	2216	17	US-10-437-963-53764	Sequence 53764, A
C 661	18	0.9	2221	17	US-10-437-963-37476	Sequence 37476, A
C 662	18	0.9	2220	17	US-10-437-963-23020	Sequence 23020, A
C 663	18	0.9	2241	17	US-10-437-963-2339	Sequence 2339, Ap
C 664	18	0.9	2241	17	US-10-437-963-8518	Sequence 8518, Ap
C 665	18	0.9	2247	17	US-10-437-963-53766	Sequence 53766, A
C 666	18	0.9	2282	18	US-10-425-115-47395	Sequence 47395, A
C 667	18	0.9	2321	18	US-10-425-115-163176	Sequence 163176, A
C 668	18	0.9	2368	18	US-10-425-115-29174	Sequence 29174, A
C 669	18	0.9	2372	18	US-10-425-115-43614	Sequence 43614, A

C 670	18	0.9	2378	17	US-10-437-963-12722	Sequence 32722, A	C 743	18	0.9	16556	15	US-10-132-720-3	Sequence 3, Appli
C 671	18	0.9	2385	15	US-10-156-761-6087	Sequence 6087, Ap	C 744	18	0.9	17491	15	US-10-017-161-1995	Sequence 1995, Ap
C 672	18	0.9	2397	17	US-10-437-963-97634	Sequence 97634, A	C 745	18	0.9	19803	15	US-10-017-161-1023	Sequence 1023, Ap
C 673	18	0.9	2415	13	US-10-011-588-36	Sequence 36, Appl	C 746	18	0.9	23871	13	US-10-087-192-703	Sequence 703, App
C 674	18	0.9	2431	9	US-09-880-107-2266	Sequence 2266, Ap	C 747	18	0.9	26429	17	US-10-322-696-106	Sequence 106, App
C 675	18	0.9	2431	16	US-10-641-643-1198	Sequence 1198, Ap	C 748	18	0.9	26991	13	US-10-087-192-24	Sequence 24, Appl
C 676	18	0.9	2433	18	US-10-425-115-26477	Sequence 26477, A	C 749	18	0.9	44288	17	US-10-367-094-23	Sequence 627, App
C 677	18	0.9	2442	16	US-10-424-599-139178	Sequence 139178, A	C 750	18	0.9	44853	17	US-10-322-281-627	Sequence 645, App
C 678	18	0.9	2451	16	US-10-424-599-95479	Sequence 95479, A	C 751	18	0.9	61791	17	US-10-322-281-645	Sequence 449, App
C 679	18	0.9	2454	15	US-10-168-09A-75	Sequence 75, Appl	C 752	18	0.9	61955	15	US-10-292-798-449	Sequence 169, App
C 680	18	0.9	2475	17	US-10-437-963-38377	Sequence 38377, A	C 753	18	0.9	67191	15	US-10-017-722-169	Sequence 1, Appli
C 681	18	0.9	2476	17	US-10-437-963-85552	Sequence 85552, A	C 754	18	0.9	87394	18	US-10-810-788A-6	Sequence 166, App
C 682	18	0.9	2526	17	US-10-437-963-38425	Sequence 38425, A	C 755	18	0.9	90351	17	US-10-367-094-166	Sequence 11, Appl
C 683	18	0.9	2527	17	US-10-437-963-1559	Sequence 1559, Ap	C 756	18	0.9	90501	15	US-10-174-020-11	Sequence 88, Appl
C 684	18	0.9	2548	16	US-10-425-115-29173	Sequence 29173, A	C 757	18	0.9	96592	11	US-09-997-722-88	Sequence 3, Appli
C 685	18	0.9	2559	16	US-10-412-699B-771	Sequence 771, App	C 758	18	0.9	98829	14	US-10-017-724-3	Sequence 1789, Ap
C 686	18	0.9	2559	13	US-10-027-632-112013	Sequence 112013, A	C 759	18	0.9	108316	15	US-10-292-798-1789	Sequence 2143, Appl
C 687	18	0.9	2591	13	US-10-027-632-112013	Sequence 112013, A	C 760	18	0.9	108316	15	US-10-017-161-2143	Sequence 12, Appl
C 688	18	0.9	2591	15	US-10-027-632-112013	Sequence 112013, A	C 761	18	0.9	113585	16	US-10-188-470-12	Sequence 82, Appl
C 689	18	0.9	2591	15	US-10-027-632-112014	Sequence 112014, A	C 762	18	0.9	127917	17	US-10-775-169-82	Sequence 3, Appli
C 690	18	0.9	2591	15	US-10-278-536-236	Sequence 236, App	C 763	18	0.9	143306	9	US-09-729-920-3	Sequence 3, Appli
C 691	18	0.9	2610	15	US-10-176-277-4	Sequence 4, Appli	C 764	18	0.9	145025	13	US-10-087-192-1051	Sequence 1051, Ap
C 692	18	0.9	2617	15	US-10-437-963-54834	Sequence 54834, A	C 765	18	0.9	145068	17	US-10-322-281-13	Sequence 33, Appl
C 693	18	0.9	2621	17	US-10-437-963-62156	Sequence 62156, A	C 766	18	0.9	174566	14	US-10-020-141-1	Sequence 37, Appl
C 694	18	0.9	2633	11	US-09-973-278-920	Sequence 920, App	C 767	18	0.9	174566	16	US-10-235-192A-37	Sequence 45, Appl
C 695	18	0.9	2646	17	US-10-437-963-10376	Sequence 10376, A	C 768	18	0.9	174566	17	US-10-322-281-45	Sequence 73, Appl
C 696	18	0.9	2655	16	US-10-424-599-57846	Sequence 57846, A	C 769	18	0.9	219352	17	US-10-322-696-73	Sequence 1627, Ap
C 697	18	0.9	2655	16	US-10-425-114-7339	Sequence 7339, Ap	C 770	18	0.9	339234	13	US-10-087-192-1627	Sequence 1, Appli
C 698	18	0.9	2655	16	US-10-425-114-7339	Sequence 7339, Ap	C 771	18	0.9	374849	13	US-10-329-960-1	Sequence 1, Appli
C 699	18	0.9	2682	14	US-10-170-656-8	Sequence 8, Appli	C 772	18	0.9	1830121	14	US-10-329-960-1	Sequence 1, Appli
C 700	18	0.9	2688	17	US-10-437-963-38454	Sequence 38454, A	C 773	18	0.9	1830121	16	US-10-158-865-1	Sequence 1, Appli
C 701	18	0.9	2706	17	US-10-437-963-7022	Sequence 7022, Ap	C 774	18	0.9	1830121	18	US-10-158-865-1	Sequence 1, Appli
C 702	18	0.9	2735	17	US-10-437-963-94592	Sequence 94592, A	C 775	18	0.9	2256646	17	US-10-470-845-1	Sequence 1, Appli
C 703	18	0.9	2820	17	US-10-437-963-76755	Sequence 76755, A	C 776	18	0.9	3673778	18	US-10-312-841-1	Sequence 1, Appli
C 704	18	0.9	2826	9	US-09-925-297-403	Sequence 293, App	C 777	18	0.9	9025608	15	US-10-156-761-1	Sequence 52076, A
C 705	18	0.9	2826	15	US-10-320-585-6930	Sequence 6930, Ap	C 778	17	0.9	25	9	US-10-098-263B-52076	Sequence 203, App
C 706	18	0.9	2829	16	US-10-320-797-131	Sequence 131, App	C 779	17	0.9	39	9	US-09-263-959-203	Sequence 11, App
C 707	18	0.9	3018	13	US-10-027-632-114681	Sequence 114681, A	C 780	17	0.9	46	10	US-09-263-959-111	Sequence 18824, A
C 708	18	0.9	3018	15	US-10-027-632-114681	Sequence 114681, A	C 781	17	0.9	60	10	US-09-908-975-18824	Sequence 3004, Ap
C 709	18	0.9	3051	18	US-10-425-115-43605	Sequence 43605, A	C 782	17	0.9	65	15	US-10-032-585-3004	Sequence 22401, A
C 710	18	0.9	3055	18	US-10-425-115-128148	Sequence 128148, A	C 783	17	0.9	98	15	US-10-029-386-22401	Sequence 17340, A
C 711	18	0.9	3092	13	US-10-027-632-264850	Sequence 264850, A	C 784	17	0.9	99	15	US-10-029-386-17340	Sequence 7305, Ap
C 712	18	0.9	3092	13	US-10-027-632-264850	Sequence 264850, A	C 785	17	0.9	114	9	US-09-969-373-786	Sequence 786, App
C 713	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A	C 786	17	0.9	117	9	US-09-864-761-22746	Sequence 22746, A
C 714	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A	C 787	17	0.9	118	9	US-09-864-761-22746	Sequence 22746, A
C 715	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A	C 788	17	0.9	121	9	US-09-728-446-572	Sequence 372, App
C 716	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A	C 789	17	0.9	121	9	US-09-728-446-572	Sequence 71916, A
C 717	18	0.9	3158	17	US-10-437-963-34020	Sequence 34020, A	C 790	17	0.9	126	16	US-10-305-720-527	Sequence 21970, A
C 718	18	0.9	3158	17	US-10-437-963-34020	Sequence 34020, A	C 791	17	0.9	126	16	US-10-305-720-527	Sequence 527, App
C 719	18	0.9	3290	17	US-10-437-963-3759	Sequence 3759, Ap	C 792	17	0.9	128	15	US-09-864-761-23270	Sequence 21970, A
C 720	18	0.9	3493	17	US-10-437-963-83811	Sequence 83811, A	C 793	17	0.9	128	15	US-10-029-386-21970	Sequence 16331, A
C 721	18	0.9	3594	17	US-10-437-963-43345	Sequence 43345, A	C 794	17	0.9	132	9	US-09-864-761-16931	Sequence 2426, A
C 722	18	0.9	3787	10	US-09-930-213-284	Sequence 284, App	C 795	17	0.9	142	16	US-10-424-599-29426	Sequence 5592, Ap
C 723	18	0.9	4080	9	US-09-833-381-922	Sequence 922, App	C 796	17	0.9	142	16	US-10-085-783A-5592	Sequence 81, Appl
C 724	18	0.9	4479	16	US-10-346-198-79	Sequence 79, Appl	C 797	17	0.9	152	10	US-09-754-853A-81	Sequence 22124, A
C 725	18	0.9	4817	10	US-09-988-462-18	Sequence 988, Informa	C 798	17	0.9	156	9	US-09-864-761-22124	Sequence 24600, A
C 726	18	0.9	4817	10	US-09-988-462-18	Sequence 988, Informa	C 799	17	0.9	157	9	US-09-864-761-24600	Sequence 26515, A
C 727	18	0.9	5677	17	US-10-788-792-45	Sequence 45, Appl	C 800	17	0.9	166	15	US-09-728-446-10	Sequence 10, Appl
C 728	18	0.9	7263	15	US-10-037-270-55	Sequence 55, Appl	C 801	17	0.9	166	15	US-09-728-446-10	Sequence 26515, A
C 729	18	0.9	7263	15	US-10-117-722-55	Sequence 55, Appl	C 802	17	0.9	167	18	US-09-969-896-6	Sequence 6, Appli
C 730	18	0.9	7791	16	US-10-375-253-35	Sequence 35, Appl	C 803	17	0.9	167	18	US-09-969-896-6	Sequence 34, Appl
C 731	18	0.9	7808	16	US-10-375-253-35	Sequence 35, Appl	C 804	17	0.9	170	17	US-10-631-958-6	Sequence 23, Appl
C 732	18	0.9	7827	15	US-10-101-510-422	Sequence 422, App	C 805	17	0.9	171	9	US-10-437-963-7372	Sequence 7372, Ap
C 733	18	0.9	7827	15	US-10-101-510-422	Sequence 422, App	C 806	17	0.9	171	9	US-10-437-963-7372	Sequence 26613, A
C 734	18	0.9	12374	15	US-10-017-161-1097	Sequence 933, App	C 807	17	0.9	174	16	US-10-424-599-115729	Sequence 115729, A
C 735	18	0.9	14770	15	US-10-292-798-933	Sequence 933, App	C 808	17	0.9	174	16	US-10-029-386-14330	Sequence 14330, A
C 736	18	0.9	14770	11	US-09-873-367C-230	Sequence 230, App	C 809	17	0.9	175	16	US-10-242-535A-369	Sequence 369, App
C 737	18	0.9	14770	11	US-09-968-007A-124	Sequence 124, App	C 810	17	0.9	175	16	US-10-085-783A-369	Sequence 1390, App
C 738	18	0.9	14770	15	US-09-968-007A-405	Sequence 405, App	C 811	17	0.9	184	9	US-09-728-446-1390	Sequence 26724, A
C 739	18	0.9	14770	15	US-10-172-118-1848	Sequence 1848, Ap	C 812	17	0.9	184	16	US-09-864-761-26724	Sequence 11, Appl
C 740	18	0.9	14770	16	US-10-342-887-1848	Sequence 1848, Ap	C 813	17	0.9	187	9	US-10-467-019-11	Sequence 27071, A
C 741	18	0.9	15439	9	US-09-764-884-36	Sequence 36, Appl	C 814	17	0.9	189	9	US-09-864-761-22687	Sequence 22687, A
C 742	18	0.9	15439	14	US-10-092-256-36	Sequence 36, Appl	C 815	17	0.9	189	9	US-09-864-761-22687	Sequence 22687, A

C 816	17	0.9	198	9	US-09-864-761-28856	Sequence 28856, A	C 889	17	0.9	349	9	US-09-864-761-4816	Sequence 4816, Ap
C 817	17	0.9	216	16	US-10-424-599-6383	Sequence 6383, Ap	C 890	17	0.9	354	18	US-10-425-115-99860	Sequence 99860, A
C 818	17	0.9	219	17	US-10-437-963-62606	Sequence 62606, A	C 891	17	0.9	357	15	US-10-116-712-14	Sequence 34, Appl
C 819	17	0.9	223	15	US-10-029-386-17312	Sequence 17312, A	C 892	17	0.9	358	16	US-10-424-599-33286	Sequence 33286, A
C 820	17	0.9	224	18	US-10-425-115-39119	Sequence 39119, A	C 893	17	0.9	360	17	US-10-437-963-70228	Sequence 70228, A
C 821	17	0.9	225	9	US-09-864-761-29376	Sequence 29376, A	C 894	17	0.9	361	9	US-09-796-692-7449	Sequence 7449, Ap
C 822	17	0.9	227	18	US-10-674-124A-6230	Sequence 6230, Ap	C 895	17	0.9	361	14	US-10-040-862-7449	Sequence 7449, Ap
C 823	17	0.9	229	17	US-10-437-963-83335	Sequence 83335, A	C 896	17	0.9	361	16	US-10-057-475B-7449	Sequence 7449, Ap
C 824	17	0.9	231	17	US-10-674-124A-865	Sequence 865, App	C 897	17	0.9	361	16	US-10-154-864B-7449	Sequence 7449, Ap
C 825	17	0.9	232	9	US-09-864-761-19928	Sequence 19928, A	C 898	17	0.9	361	17	US-10-154-864B-7449	Sequence 7449, Ap
C 826	17	0.9	233	9	US-09-923-876-17	Sequence 17, Appl	C 899	17	0.9	363	14	US-10-764-324-7449	Sequence 7449, Ap
C 827	17	0.9	233	10	US-09-923-876-17	Sequence 17, Appl	C 900	17	0.9	363	14	US-10-231-411-3	Sequence 3, Appl1
C 828	17	0.9	234	9	US-09-864-761-19661	Sequence 19661, A	C 901	17	0.9	363	17	US-10-437-963-73118	Sequence 73118, A
C 829	17	0.9	234	17	US-10-437-963-76619	Sequence 76619, A	C 902	17	0.9	366	18	US-10-425-115-11446	Sequence 11446, Ap
C 830	17	0.9	241	16	US-10-424-599-90106	Sequence 90106, A	C 903	17	0.9	367	18	US-10-674-124A-6506	Sequence 19282, A
C 831	17	0.9	242	9	US-09-864-761-19088	Sequence 19088, A	C 904	17	0.9	368	17	US-10-767-701-19282	Sequence 964, App
C 832	17	0.9	242	9	US-09-864-761-19088	Sequence 19088, A	C 905	17	0.9	370	16	US-09-917-800A-964	Sequence 964, App
C 833	17	0.9	243	18	US-10-425-115-141816	Sequence 141816, A	C 906	17	0.9	370	16	US-10-388-934-675	Sequence 675, App
C 834	17	0.9	245	9	US-09-864-761-28392	Sequence 28392, A	C 907	17	0.9	370	16	US-10-191-803-761	Sequence 761, App
C 835	17	0.9	248	18	US-10-425-115-49645	Sequence 49645, A	C 908	17	0.9	370	16	US-10-152-319A-1093	Sequence 1093, Ap
C 836	17	0.9	257	18	US-10-674-124A-12500	Sequence 12500, A	C 909	17	0.9	372	11	US-09-864-761-22031	Sequence 22031, A
C 837	17	0.9	258	15	US-10-029-386-14589	Sequence 14589, A	C 910	17	0.9	372	11	US-09-987-899-5440	Sequence 5440, Ap
C 838	17	0.9	260	17	US-10-437-963-40217	Sequence 40217, A	C 911	17	0.9	374	16	US-10-424-599-136304	Sequence 136304, A
C 839	17	0.9	260	18	US-10-674-124A-977	Sequence 977, App	C 912	17	0.9	376	9	US-10-767-701-20802	Sequence 20802, A
C 840	17	0.9	261	9	US-09-864-761-17114	Sequence 17114, App	C 913	17	0.9	377	10	US-09-864-761-26681	Sequence 26681, A
C 841	17	0.9	261	11	US-09-732-627A-3060	Sequence 3060, App	C 914	17	0.9	377	10	US-09-918-995-29709	Sequence 29709, A
C 842	17	0.9	264	15	US-10-029-386-20098	Sequence 20098, A	C 915	17	0.9	380	18	US-10-425-115-60266	Sequence 60266, A
C 843	17	0.9	264	17	US-10-437-963-16656	Sequence 16656, A	C 916	17	0.9	381	9	US-09-864-761-2610	Sequence 2610, A
C 844	17	0.9	270	9	US-09-294-093B-2493	Sequence 2493, App	C 917	17	0.9	382	18	US-10-425-115-51260	Sequence 51260, A
C 845	17	0.9	270	14	US-10-062-727-854	Sequence 854, App	C 918	17	0.9	382	18	US-10-425-115-182580	Sequence 182580, A
C 846	17	0.9	270	17	US-10-437-963-59361	Sequence 59361, A	C 919	17	0.9	383	14	US-10-101-464A-393	Sequence 393, App
C 847	17	0.9	274	16	US-10-424-599-12626	Sequence 12626, A	C 920	17	0.9	383	16	US-10-424-599-2328	Sequence 2328, App
C 848	17	0.9	274	17	US-10-437-963-62146	Sequence 62146, A	C 921	17	0.9	384	18	US-10-674-124A-25152	Sequence 25152, A
C 849	17	0.9	274	18	US-10-425-115-149550	Sequence 149550, A	C 922	17	0.9	384	14	US-10-062-727-941	Sequence 941, App
C 850	17	0.9	276	9	US-09-864-761-17651	Sequence 17651, A	C 923	17	0.9	385	17	US-10-767-795-3189	Sequence 3189, App
C 851	17	0.9	276	18	US-10-674-124A-23224	Sequence 23224, A	C 924	17	0.9	388	18	US-10-674-124A-5946	Sequence 5946, App
C 852	17	0.9	280	13	US-10-062-727-822	Sequence 822, App	C 925	17	0.9	388	18	US-10-425-115-8123	Sequence 8123, Ap
C 853	17	0.9	282	14	US-10-027-632-273128	Sequence 273128, A	C 926	17	0.9	390	16	US-10-132-812-13	Sequence 13, Appl
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C 972	17	0.9	422	16	US-10-424-599-87353
C 973	17	0.9	424	18	US-10-425-115-1193
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C 991	17	0.9	442	18	US-10-674-124A-25514
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ALIGNMENTS

RESULT 1
 US-10-086-464-1
 ; Sequence 1, Application US/10086464
 ; Publication No. US20020199218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GORING, Daphne R. et al.
 ; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
 ; FILE REFERENCE: P 25,762-A USA
 ; CURRENT APPLICATION NUMBER: US/10/086,464
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 10/069,304
 ; PRIOR FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: PCT/CA00/00966
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/149,466
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: US 60/159,122
 ; PRIOR FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1944
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1944)
 US-10-086-464-1

Sequence 7663, Ap
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 Sequence 29080, A
 Sequence 565, App
 Sequence 105, App
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 Sequence 3954, Ap
 Sequence 98678, A
 Sequence 87353, A
 Sequence 1193, Ap
 Sequence 9485, Ap
 Sequence 9486, Ap
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 Sequence 866, App
 Sequence 867, App
 Sequence 868, App
 Sequence 15013, A
 Sequence 14336, A
 Sequence 12426, A
 Sequence 70947, A
 Sequence 46785, A
 Sequence 5616, Ap
 Sequence 21413, A
 Sequence 140627, A
 Sequence 25190, A
 Sequence 48033, A
 Sequence 25514, A
 Sequence 79382, A
 Sequence 5262, Ap
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 Sequence 76, App1
 Sequence 92, App1
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 Sequence 100953, A

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841	TTAG	900		
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RESULT 2

US-10-086-464-3
; Sequence 3, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464

; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2189
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2189)
; OTHER INFORMATION:
US-10-086-464-3

Query Match 100.0%; Score 1944; DB 13; Length 2189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 217 CCATCCATATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276
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QY 241 CCGCTCTCACTAGCGCCCGGATCTCACCCGACCTGTTACTCTCTCTCTCTCTCTCTCT 300
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QY 301 CCACCTTCACTAGCGCCCGGATCTCACCCGACCTGTTACTCTCTCTCTCTCTCTCTCT 360
Db 397 CCACCTTCACTAGCGCCCGGATCTCACCCGACCTGTTACTCTCTCTCTCTCTCTCTCT 456
QY 361 CCATCTTCT 420
Db 457 CCATCTTCT 516
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Db 577 AAGAAGAAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 636
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Db 697 AACACCGGTGATGATGCTGTAAGTCTCACTTACCAACCACTTAAAGCTTCACTTCA 756
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Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
US-09-923-876-5096
; Sequence 5096, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghumath V.
; APPLICANT: Kamigaki, Laura Y. (lto)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 5096
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456354H1
; NAME/KEY: unsure
; LOCATION: 63
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5096

Query Match
Best Local Similarity 1.3%; Score 26; DB 10; Length 268;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 203 TTGAAGCTAAGTTGCTGATTTGG 228

RESULT 6
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; Sequence 5803, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 5803
; LENGTH: 808
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS25481_1
US-10-767-701-5803

Query Match
Best Local Similarity 1.3%; Score 26; DB 17; Length 808;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTGAAGCTAAGTTGCTGATTTGG 1256
DB 680 TTGAAGCTAAGTTGCTGATTTGG 705

RESULT 7
US-10-425-114-1922
; Sequence 1922, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1922
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700171392_FLI
US-10-425-114-1922

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 951;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTGAAGCTAAGTTGCTGATTTGG 1256
DB 16 TTGAAGCTAAGTTGCTGATTTGG 41

RESULT 8
US-10-425-114-13131
; Sequence 13131, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13131
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-GMFL02220096D10_FLI
US-10-425-114-13131

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1011;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 GAGAGCTGAGCTTTTCATTTGG 1385
DB 246 GAGAGCTGAGCTTTTCATTTGG 271

```
RESULT 9
US-10-425-115-143424
; Sequence 143424, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 143424
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_6227C.1
US-10-425-115-143424

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1100;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTGAAGCTAAGTGTGCTGATTTTGG 1256
DB 222 TTGAAGCTAAGTGTGCTGATTTTGG 247

RESULT 10
US-10-425-114-36420
; Sequence 36420, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36420
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMKOTEOSINTE097B02_FLI
US-10-425-114-36420

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1134;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTGAAGCTAAGTGTGCTGATTTTGG 1256
DB 260 TTGAAGCTAAGTGTGCTGATTTTGG 285

RESULT 11
US-10-425-114-6300
; Sequence 6300, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
```

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6300
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700560157_FLI
US-10-425-114-6300

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1500;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 GAGAAGCTGACGTTTCTCATTTGG 1385
DB 779 GAGAAGCTGACGTTTCTCATTTGG 804

RESULT 12
US-10-424-599-47702
; Sequence 47702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 47702
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_143080C.1
US-10-424-599-47702

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1552;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 GAGAAGCTGACGTTTCTCATTTGG 1385
DB 779 GAGAAGCTGACGTTTCTCATTTGG 804

RESULT 13
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
```



```

; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326

```

```

Query Match      1.3%; Score 26; DB 16; Length 1724;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1231 TTGAAGCTAAGTTGCTGATTTGG 1256
Db      832 TTGAAGCTAAGTTGCTGATTTGG 857

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RESULT 14
US-10-425-115-57011
; Sequence 57011, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 57011
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_151984C.1
US-10-425-115-57011

```

```

Query Match      1.3%; Score 26; DB 18; Length 2886;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1231 TTGAAGCTAAGTTGCTGATTTGG 1256
Db      1886 TTGAAGCTAAGTTGCTGATTTGG 1911

```

```

RESULT 15
US-10-425-115-72287
; Sequence 72287, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 72287
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure

```

```

; LOCATION: (1)..(682)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165926C.1
US-10-425-115-72287

```

```

Query Match      1.3%; Score 25; DB 18; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      669 ACCTCTCCACCTCCACCAACGCGCT 693
Db      391 ACCTCTCCACCTCCACCAACGCGCT 415

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Search completed: November 13, 2004, 17:11:15
Job time : 727 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 12:24:05 ; Search time 4166 Seconds

(without alignments)
17004.042 Million cell updates/sec

Title: US-10-069-304-1

Perfect score: 1944
Sequence: 1 atgtccctcgcgcgcgtctcc.....atagtgcacctctctttaa 1944

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 32822875 segs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	429	22.1	723	6	CD839231 RPO2.1141
2	273	14.0	453	8	BH442220 BOCJLN68TR
3	187	9.6	753	8	B2455058 BOKKA33TF
4	66	3.4	853	5	BX834233 BX834233
5	66	3.4	2106	3	CNSO4QX
6	65	3.3	314	6	CD811645
7	65	3.3	314	6	CD811912
8	53	2.7	561	1	AVS39333
9	53	2.7	584	1	AVS43493
10	42	2.2	754	8	BH432371
11	32	1.6	342	8	B2456327
12	30	1.5	744	8	B2066106
13	30	1.5	925	8	CL469889
14	29	1.5	472	7	CO066237
15	29	1.5	505	4	BM061076
16	29	1.5	573	1	AVS51753
17	29	1.5	607	9	CC968148
18	29	1.5	620	8	BH577077
19	29	1.5	651	5	BH043317
20	29	1.5	695	5	BH928300
21	29	1.5	1036	5	BX837083
22	28	1.4	713	5	BP175991
23	27	1.4	315	5	BP752316
24	27	1.4	414	8	BH434903

C 25	27	1.4	536	1	AL369682	AL369682
C 26	26	1.3	294	6	CD004164	CD004164
C 27	26	1.3	295	7	F14384	F14384
C 28	26	1.3	356	1	AV547061	AV547061
C 29	26	1.3	358	1	BP592641	BP592641
C 30	26	1.3	360	1	AV534188	AV534188
C 31	26	1.3	361	5	BP603573	BP603573
C 32	26	1.3	395	1	AV819894	AV819894
C 33	26	1.3	399	1	AV797870	AV797870
C 34	26	1.3	402	1	AV800600	AV800600
C 35	26	1.3	411	1	AV799812	AV799812
C 36	26	1.3	421	1	AV810018	AV810018
C 37	26	1.3	427	1	AV788292	AV788292
C 38	26	1.3	430	1	AV795981	AV795981
C 39	26	1.3	436	1	AV793009	AV793009
C 40	26	1.3	439	1	AV819129	AV819129
C 41	26	1.3	439	1	BP604880	BP604880
C 42	26	1.3	444	5	BP589597	BP589597
C 43	26	1.3	459	1	AV538962	AV538962
C 44	26	1.3	482	5	BH820923	BH820923
C 45	26	1.3	484	4	BG817458	BG817458
C 46	26	1.3	593	2	BR176907	BR176907
C 47	26	1.3	595	6	CF015663	CF015663
C 48	26	1.3	613	6	CF232052	CF232052
C 49	26	1.3	637	5	BQ134241	BQ134241
C 50	26	1.3	641	6	CA248316	CA248316
C 51	26	1.3	645	5	BQ506689	BQ506689
C 52	26	1.3	666	5	BH499754	BH499754
C 53	26	1.3	669	7	CO373192	CO373192
C 54	26	1.3	673	6	CA164704	CA164704
C 55	26	1.3	682	6	CA095337	CA095337
C 56	26	1.3	750	6	CA148443	CA148443
C 57	26	1.3	757	4	BS596561	BS596561
C 58	26	1.3	759	4	BM408099	BM408099
C 59	26	1.3	824	6	CD435142	CD435142
C 60	26	1.3	857	6	CA175432	CA175432
C 61	26	1.3	867	9	CL512079	CL512079
C 62	26	1.3	899	7	CK096498	CK096498
C 63	26	1.3	1053	3	AY108241	AY108241
C 64	25	1.3	373	5	BP655346	BP655346
C 65	25	1.3	679	8	BH986592	BH986592
C 66	25	1.3	770	8	BH986592	BH986592
C 67	25	1.3	863	6	CA102987	CA102987
C 68	25	1.3	875	9	CG333037	CG333037
C 69	24	1.2	308	1	AU101108	AU101108
C 70	24	1.2	342	1	AV518408	AV518408
C 71	24	1.2	388	1	AU083425	AU083425
C 72	24	1.2	523	2	AM682900	AM682900
C 73	24	1.2	527	7	CF442220	CF442220
C 74	24	1.2	578	1	AV589114	AV589114
C 75	24	1.2	694	7	CK242595	CK242595
C 76	24	1.2	782	8	BH581217	BH581217
C 77	24	1.2	795	5	BQ506870	BQ506870
C 78	24	1.2	799	7	CK242598	CK242598
C 79	24	1.2	922	7	CK279503	CK279503
C 80	24	1.2	955	6	CA473990	CA473990
C 81	23	1.2	171	1	AJ452111	AJ452111
C 82	23	1.2	229	2	AM375078	AM375078
C 83	23	1.2	254	6	CB263837	CB263837
C 84	23	1.2	300	1	AV525199	AV525199
C 85	23	1.2	324	7	AM830192	AM830192
C 86	23	1.2	331	5	F14383	F14383
C 87	23	1.2	344	7	BQ901492	BQ901492
C 88	23	1.2	382	1	AV550142	AV550142
C 89	23	1.2	407	5	BP605853	BP605853
C 90	23	1.2	430	1	A1461081	A1461081
C 91	23	1.2	440	1	AV825650	AV825650
C 92	23	1.2	444	6	CA213655	CA213655
C 93	23	1.2	445	6	CB258929	CB258929
C 94	23	1.2	452	1	AV793973	AV793973
C 95	23	1.2	460	4	BG727065	BG727065
C 96	23	1.2	480	5	EX482428	EX482428
C 97	23	1.2	482	7	CN041102	CN041102

C 98	23	1.2	487	7	H99218	H99218 yx21a01.s1	171	22	1.1	563	6	CA233012	CA233012	SCRUPFL306
C 99	23	1.2	489	2	AM982145	AM982145 SSS0075.S	C 172	22	1.1	565	2	AM753578	AM753578	PM2-CT026
C 100	23	1.2	498	2	AM454236	AM454236 B2300015A	C 173	22	1.1	574	7	CF416485	CF416485	lr_LCIED
C 101	23	1.2	502	4	BG369831	BG369831 HVSME1002	C 174	22	1.1	591	6	CF023990	CF023990	OB812612
C 102	23	1.2	515	2	AM418529	AM418529 xc32c08.x	C 175	22	1.1	597	1	AJ453318	AJ453318	AJ453318
C 103	23	1.2	522	5	BU288421	BU288421 603604609	C 176	22	1.1	617	6	CB883350	CB883350	HO01P13w
C 104	23	1.2	522	1	A1729561	A1729561 BNLGH1136	C 177	22	1.1	629	9	CL193146	CL193146	CS156619
C 105	23	1.2	525	4	BG448469	BG448469 NF036E04R	C 178	22	1.1	632	9	CF415989	CF415989	lr_LCIED
C 106	23	1.2	529	4	BE637850	BE637850 WHE1755-1	C 179	22	1.1	636	7	CF839242	CF839242	GH_MBD000
C 107	23	1.2	530	1	AV554582	AV554582 AY554582	C 180	22	1.1	648	8	BH022712	BH022712	GA_EBD010
C 108	23	1.2	531	6	CA393582	CA393582 c839h10.Y	C 181	22	1.1	667	5	BQ407542	BQ407542	GA_E5502
C 109	23	1.2	534	2	AM375080	AM375080 QV1-CT011	C 182	22	1.1	676	1	AJ455502	AJ455502	AJ455502
C 110	23	1.2	534	6	CA233016	CA233016 SCRUPFL306	C 183	22	1.1	677	6	CA927407	CA927407	MTU6CR.P8
C 111	23	1.2	535	5	CD922858	CD922858 G750.105F	C 184	22	1.1	680	1	AJ454164	AJ454164	AJ454164
C 112	23	1.2	542	5	BO316487	BO316487 QV1-CT011	C 185	22	1.1	685	7	CF809983	CF809983	lr_LCIED
C 113	23	1.2	550	2	AM134475	AM134475 UI-H-BT1-	C 186	22	1.1	690	1	AJ446992	AJ446992	AJ446992
C 114	23	1.2	557	5	BQ315895	BQ315895 QV1-CT011	C 187	22	1.1	691	6	CA237152	CA237152	SCMCFPL500
C 115	23	1.2	572	2	BF042118	BF042118 BP250021B	C 188	22	1.1	694	9	CL172776	CL172776	OGA043TC
C 116	23	1.2	573	4	BM815391	BM815391 EST593485	C 189	22	1.1	698	8	BZ524377	BZ524377	OGA043TC
C 117	23	1.2	575	4	BI786430	BI786430 sai49a07.	C 190	22	1.1	705	9	CG069019	CG069019	PUPVR95TB
C 118	23	1.2	578	5	BO316490	BO316490 QV1-CT011	C 191	22	1.1	707	7	CO046736	CO046736	lr_LCICF
C 119	23	1.2	585	1	AI1999650	AI1999650 QV1556869	C 192	22	1.1	714	9	CG069020	CG069020	PUPVR95TD
C 120	23	1.2	584	5	BP131083	BP131083 BP131083	C 193	22	1.1	718	7	CF415958	CF415958	lr_LCIED
C 121	23	1.2	586	1	AV832259	AV832259 AV832259	C 194	22	1.1	731	1	AJ448495	AJ448495	AJ448495
C 122	23	1.2	596	2	AM617255	AM617255 EST323666	C 195	22	1.1	735	1	AJ445542	AJ445542	AJ445542
C 123	23	1.2	596	2	BO316492	BO316492 QV1-CT011	C 196	22	1.1	740	8	BH690594	BH690594	BOMAV47TF
C 124	23	1.2	597	6	CA215962	CA215962 SCGFPL401	C 197	22	1.1	741	8	BH550760	BH550760	BOGSV5STR
C 125	23	1.2	608	2	AM033109	AM033109 EST276668	C 198	22	1.1	743	1	AJ451397	AJ451397	AJ451397
C 126	23	1.2	608	4	BM814985	BM814985 EST593079	C 199	22	1.1	756	8	CG387007	CG387007	PURHP31TD
C 127	23	1.2	610	6	CA237191	CA237191 SCJFPL1C0	C 200	22	1.1	760	1	AJ454727	AJ454727	AJ454727
C 128	23	1.2	611	6	CA237156	CA237156 SCMCFPL500	C 201	22	1.1	801	1	AJ446803	AJ446803	AJ446803
C 129	23	1.2	618	1	AV826238	AV826238 AV826238	C 202	22	1.1	860	7	CK202584	CK202584	FGAS01110
C 130	23	1.2	628	1	BI067795	BI067795 PG51n.PK0	C 203	22	1.1	875	9	CG036507	CG036507	PUPVR95TD
C 131	23	1.2	628	4	BI067795	BI067795 PG51n.PK0	C 204	22	1.1	885	9	CG046981	CG046981	BOMV47TF
C 132	23	1.2	646	8	BH480820	BH480820 BOHLZ45TF	C 205	22	1.1	895	9	CG046981	CG046981	BOMV47TF
C 133	23	1.2	669	6	CA247444	CA247444 SCCCFPL505	C 206	22	1.1	933	5	BX416490	BX416490	BOMV47TF
C 134	23	1.2	674	6	CA298046	CA298046 SCMCFPL802	C 207	22	1.1	935	8	BZ465289	BZ465289	FGAS01110
C 135	23	1.2	695	9	CE670069	CE670069 LIQT-G8S-	C 208	22	1.1	1020	8	BZ465289	BZ465289	FGAS01110
C 136	23	1.2	696	9	CE670069	CE670069 LIQT-G8S-	C 209	22	1.1	1224	4	BI178502	BI178502	EST519447
C 137	23	1.2	697	6	CA066727	CA066727 SCJFPL401	C 210	22	1.1	242	4	BI178502	BI178502	EST519447
C 138	23	1.2	700	8	BH550441	BH550441 BOMZ722TF	C 211	22	1.1	270	2	BH552920	BH552920	EST519447
C 139	23	1.2	710	1	A1302817	A1302817 qn58h01.x	C 212	22	1.1	271	2	BE921790	BE921790	EST425559
C 140	23	1.2	715	5	BU099573	BU099573 WHE3309.A	C 213	22	1.1	330	5	BU672062	BU672062	Hah13.He
C 141	23	1.2	724	8	BH569945	BH569945 BOHME63TR	C 214	22	1.1	341	7	CF860127	CF860127	ps2G008XL
C 142	23	1.2	729	8	BH982856	BH982856 odf13fE09.	C 215	22	1.1	341	7	CF860127	CF860127	ps2G008XL
C 143	23	1.2	731	5	CB655196	CB655196 OSJNEC08F	C 216	22	1.1	370	1	A1354035	A1354035	zen1307.s
C 144	23	1.2	736	5	BU595386	BU595386 AGENCOURT	C 217	22	1.1	370	7	CN577574	CN577574	rf41f04.x
C 145	23	1.2	745	1	AJ452950	AJ452950 AJ452950	C 218	22	1.1	373	5	EX303069	EX303069	EX303069
C 146	23	1.2	750	5	BU302060	BU302060 603739336	C 219	22	1.1	373	5	EX303069	EX303069	EX303069
C 147	23	1.2	764	1	AJ395192	AJ395192 AJ395192	C 220	22	1.1	382	1	CD231397	CD231397	SS1_16.BO
C 148	23	1.2	765	5	BH240528	BH240528 603321372	C 221	22	1.1	388	1	A1486438	A1486438	EST244759
C 149	23	1.2	781	7	CN793280	CN793280 4128280.B	C 222	22	1.1	390	7	CK460812	CK460812	931126.MA
C 150	23	1.2	782	5	BU354003	BU354003 603528466	C 223	22	1.1	392	7	CK460812	CK460812	931126.MA
C 151	23	1.2	786	5	BZ069046	BZ069046 1Kf36T01.	C 224	22	1.1	395	6	CD060623	CD060623	RZ147A1E1
C 152	23	1.2	792	8	BH601781	BH601781 BOHRD80TR	C 225	22	1.1	402	4	BN030863	BN030863	Bj300863
C 153	23	1.2	811	7	CN232862	CN232862 WLA054E11	C 226	22	1.1	404	7	CN035495	CN035495	nm_5.O16
C 154	23	1.2	825	7	CN242228	CN242228 WLA054E11	C 227	22	1.1	405	7	CN035495	CN035495	nm_5.O16
C 155	23	1.2	869	7	CK205169	CK205169 FGAS01370	C 228	22	1.1	409	7	R022717	R022717	Y880H05.r1
C 156	23	1.2	872	6	CA268425	CA268425 SCOSRT305	C 229	22	1.1	411	7	RO22717	RO22717	Y880H05.r1
C 157	23	1.2	933	9	AM982539	AM982539 HVSMB9000	C 230	22	1.1	413	7	BE436813	BE436813	EST407931
C 158	23	1.2	955	9	AG079376	AG079376 Pan_tlog1	C 231	22	1.1	413	7	BE436813	BE436813	EST407931
C 159	23	1.2	1009	6	CA252912	CA252912 SCBFFL114	C 232	22	1.1	416	1	AA325689	AA325689	Y880H05.r1
C 160	23	1.2	1114	6	CA278955	CA278955 SCBFFL114	C 233	22	1.1	422	6	CD847034	CD847034	DHOAB53ZH
C 161	23	1.2	1257	8	BZ675184	BZ675184 PUBEX87TD	C 234	22	1.1	424	5	BO916616	BO916616	QHB18H19.
C 162	22	1.1	276	1	AV008495	AV008495 AV008495	C 235	22	1.1	424	5	BO916616	BO916616	QHB18H19.
C 163	22	1.1	416	5	BP652725	BP652725 BP652725	C 236	22	1.1	424	5	BO916616	BO916616	QHB18H19.
C 164	22	1.1	433	5	AV791845	AV791845 AV791845	C 237	22	1.1	451	7	CN045547	CN045547	v11_p6.F
C 165	22	1.1	473	5	BU818693	BU818693 UA33CPD12	C 238	22	1.1	457	6	CD210897	CD210897	HS1_66.F0
C 166	22	1.1	490	4	BM358085	BM358085 GA_Ea000	C 239	22	1.1	458	7	RE59533	RE59533	y782d11.r1
C 167	22	1.1	499	4	CD733903	CD733903 4046928.1	C 240	22	1.1	459	1	AU249221	AU249221	AU249221
C 168	22	1.1	524	6	CF799817	CF799817 lr_PARCFC	C 241	22	1.1	459	1	AU249221	AU249221	AU249221
C 169	22	1.1	529	7	BZ620930	BZ620930 1966h07.B	C 242	22	1.1	459	1	AU249221	AU249221	AU249221
C 170	22	1.1	557	8	BZ620930	BZ620930 1966h07.B	C 243	22	1.1	459	9	AG225635	AG225635	Lotus.COR

C 244	21	1.1	461	7	CN038230	nm_26_b9	317	21	1.1	725	7	CN358608	CN358608	170005999
C 245	21	1.1	462	7	CN037727	nm_23_x6	C 318	21	1.1	739	6	CD285334	CD285334	G39164.86
C 246	21	1.1	465	7	CN042020	nm_36h_j2	C 319	21	1.1	741	4	BI936018	BI936018	EST555907
C 247	21	1.1	465	7	CN469507	hh_Ab_Bra	C 320	21	1.1	746	3	CN509218	CN509218	Single re
C 248	21	1.1	470	7	CN036285	nm_14_15	C 321	21	1.1	751	7	CK720191	CK720191	20574 SwO
C 249	21	1.1	483	5	BO618122	fa56d10	C 322	21	1.1	753	8	BZ636310	BZ636310	OGAMS847C
C 250	21	1.1	483	7	CN043940		C 323	21	1.1	754	3	CN509217	CN509217	Single re
C 251	21	1.1	483	7	R53242		C 324	21	1.1	755	7	CO078179	CO078179	GR_Ba0P
C 252	21	1.1	494	1	AI771280	EST522296	C 325	21	1.1	757	8	BZ636313	BZ636313	OGAMS847M
C 253	21	1.1	494	4	BG447806	NE103A08E	C 326	21	1.1	770	5	BP753955	BP753955	BP753955
C 254	21	1.1	500	5	BQ262101	EST270H01.Y	C 327	21	1.1	774	5	EX683535	EX683535	EX683535
C 255	21	1.1	504	7	CK452686	909487.MA	C 328	21	1.1	777	7	CK720267	CK720267	20668 SwO
C 256	21	1.1	505	7	CK453752		C 329	21	1.1	778	9	CN5042M4	CN5042M4	Tetraodon
C 257	21	1.1	505	7	CN037461	nm_22_2_d	C 330	21	1.1	787	9	AG529449	AG529449	Mus muscu
C 258	21	1.1	505	7	W86386	zh55d06.it	C 331	21	1.1	795	4	BI935482	BI935482	BI935482
C 259	21	1.1	506	7	CN040216	nm_35h_d8	C 332	21	1.1	804	4	BI753284	BI753284	60302615
C 260	21	1.1	510	7	CN038799	nm_29_110	C 333	21	1.1	806	3	CN509637	CN509637	Single re
C 261	21	1.1	511	7	CK460107	930358.MA	C 334	21	1.1	807	9	CC739159	CC739159	CG739159
C 262	21	1.1	515	5	CR348709	Medicago	C 335	21	1.1	813	4	BG257479	BG257479	BMEM1177R
C 263	21	1.1	516	9	CR348709		C 336	21	1.1	813	4	BG545818	BG545818	602573096
C 264	21	1.1	526	6	CD060102	MA1-0006G	C 337	21	1.1	813	8	CC118014	CC118014	NDL_20D21
C 265	21	1.1	531	7	AL702099	DKFZP686B	C 338	21	1.1	827	9	CC733843	CC733843	OGKRA697H
C 266	21	1.1	534	7	CK306048	ij99G01.Y	C 339	21	1.1	828	6	CA473587	CA473587	AGENCOURT
C 267	21	1.1	536	7	CN044440	v11_P51.h	C 340	21	1.1	835	9	CG925944	CG925944	MBEM1177R
C 268	21	1.1	539	6	CR210498		C 341	21	1.1	844	9	CG226899	CG226899	OGXBG177H
C 269	21	1.1	542	8	BH882334	hw36906.b	C 342	21	1.1	847	7	CO806421	CO806421	AGENCOURT
C 270	21	1.1	545	5	BQ267225	ij99G01.Y	C 343	21	1.1	850	5	BO797643	BO797643	EST_6581
C 271	21	1.1	545	1	AW933703	EST359546	C 344	21	1.1	863	9	CL207367	CL207367	ZMHB055
C 272	21	1.1	555	2	AI896248	EST265691	C 345	21	1.1	892	4	BG193644	BG193644	RST12778
C 273	21	1.1	557	2	BI847496	469344.MA	C 346	21	1.1	903	9	CG312007	CG312007	CG312007
C 274	21	1.1	561	2	AM655748	106986.MA	C 347	21	1.1	914	9	CG246610	CG246610	OGXDM51TV
C 275	21	1.1	562	5	BQ263817	Iaai18d11.	C 348	21	1.1	920	7	CR244611	CR244611	EST728248
C 276	21	1.1	564	8	BZ626373	ih45d09.b	C 349	21	1.1	921	3	CR705904	CR705904	Tetraodon
C 277	21	1.1	565	1	AU261086	AU261086	C 350	21	1.1	926	5	BX409971	BX409971	BX409971
C 278	21	1.1	573	4	BM380272	MEST517-F	C 351	21	1.1	933	7	CK254592	CK254592	EST738229
C 279	21	1.1	579	5	BU079690	946146F03	C 352	21	1.1	947	7	BT748877	BT748877	CH34024.A
C 280	21	1.1	589	7	CN042561	v11_P43.b	C 353	21	1.1	947	7	CN020825	CN020825	AGENCOURT
C 281	21	1.1	591	2	BP242782	601877666	C 354	21	1.1	948	7	CK246533	CK246533	EST730170
C 282	21	1.1	594	2	BX306879	BX306879	C 355	21	1.1	964	8	CC426175	CC426175	PURHOA47D
C 283	21	1.1	595	1	AJ801887	BP135468	C 356	21	1.1	967	4	BM466173	BM466173	AGENCOURT
C 284	21	1.1	597	5	BP135468	OGI9G14.Y	C 357	21	1.1	997	3	CN5095H4	CN5095H4	Single re
C 285	21	1.1	599	2	BO875889	BO875889	C 358	21	1.1	999	4	CK251691	CK251691	EST735328
C 286	21	1.1	601	2	BE573288	602079661.Y	C 359	21	1.1	1015	4	BM469078	BM469078	AGENCOURT
C 287	21	1.1	602	6	CD847727	CD847727	C 360	21	1.1	1024	3	CN5095H3	CN5095H3	Single re
C 288	21	1.1	603	6	CD846661	BE460504	C 361	21	1.1	1067	9	CN5060YO	CN5060YO	Single re
C 289	21	1.1	605	2	BE460504	EST411923	C 362	21	1.1	1127	5	BO067073	BO067073	AGENCOURT
C 290	21	1.1	606	7	CF858767	CF858767	C 363	21	1.1	1135	9	AT413691	AT413691	Homo sapi
C 291	21	1.1	609	3	CR714685	CR714685	C 364	21	1.1	1365	9	AT413692	AT413692	Pan trogl
C 292	21	1.1	616	7	CN045792	602079661.Y	C 365	21	1.1	1413	3	CL493616	CL493616	SAIT_581
C 293	21	1.1	619	4	BG389914	602414105	C 366	21	1.1	1423	9	CR692038	CR692038	Tetraodon
C 294	21	1.1	622	6	CA831327	CA831327	C 367	21	1.1	1433	3	CL493616	CL493616	SAIT_581
C 295	21	1.1	627	6	CA523309	KS12020H0	C 368	21	1.1	1433	3	CR687873	CR687873	Tetraodon
C 296	21	1.1	629	5	BU624937	UI-H-FG1-	C 369	21	1.1	1437	3	CR686868	CR686868	Tetraodon
C 297	21	1.1	629	7	CN040661	nm_37h_j8	C 370	21	1.1	1444	3	CR692070	CR692070	Tetraodon
C 298	21	1.1	637	5	BO408233	GA_Ed000	C 371	21	1.1	1456	3	CR729013	CR729013	Tetraodon
C 299	21	1.1	639	4	BI178518	EST519463	C 372	21	1.1	1955	3	CN50A1NN	CN50A1NN	Arabidops
C 300	21	1.1	640	5	BQ408325	BQ408325	C 373	21	1.1	2041	3	CN509Z04	CN509Z04	Arabidops
C 301	21	1.1	641	5	BQ409216	GA_Ed001	C 374	21	1.1	2151	3	CR615699	CR615699	Full-1eng
C 302	21	1.1	646	5	BQ390080	NISC mg11	C 375	20	1.0	116	2	BR737616	BR737616	PM1-KT003
C 303	21	1.1	655	6	CD828414	CD828414	C 376	20	1.0	141	1	AT131853	AT131853	Arabidops
C 304	21	1.1	665	5	BU575172	BU575172	C 377	20	1.0	169	8	CC053712	CC053712	SALK_0470
C 305	21	1.1	666	5	BQ416196	GA_Ed010	C 378	20	1.0	179	1	AB603482	AB603482	Mus muscu
C 306	21	1.1	666	8	AQ329920	gdXbD045P	C 379	20	1.0	187	5	BO904735	BO904735	Ta04_06h1
C 307	21	1.1	669	3	CNS09630	Single re	C 380	20	1.0	200	7	CN851169	CN851169	001001AIF
C 308	21	1.1	674	6	CD837334	BN45_051N	C 381	20	1.0	200	7	D40842	D40842	RICS013A.R
C 309	21	1.1	677	8	BH998130	oe497b01	C 382	20	1.0	204	4	BZ683398	BZ683398	Bu683398
C 310	21	1.1	680	7	CNS47578	EST_16856	C 383	20	1.0	210	9	CG343415	CG343415	OG343415
C 311	21	1.1	683	4	BZ307836	BZ307836	C 384	20	1.0	213	1	AI254819	AI254819	qv34F08.x
C 312	21	1.1	702	4	BI922743	BI922743	C 385	20	1.0	215	7	D40889	D40889	RICS3070A.R
C 313	21	1.1	712	4	CO074694	GR_Ea340	C 386	20	1.0	215	8	AZ310248	AZ310248	IM0025E11
C 314	21	1.1	718	4	BM407268	EST581595	C 387	20	1.0	216	7	D40962	D40962	RICS3167A.R
C 315	21	1.1	719	5	BX085686	BX085686	C 388	20	1.0	220	7	CN490249	CN490249	MDfW2016C
C 316	21	1.1	719	7	CF571601	MC5015605	C 389	20	1.0	223	5	BP746939	BP746939	BP746939

C 390	20	1.0	226	2	AW268259	xt34e07.x	C 463	20	1.0	442	2	BF933983	BF933983	IL5-NT022
C 391	20	1.0	226	6	C97797	Rice	C 464	20	1.0	443	1	AUI62019	AUI62019	ARI62019
C 392	20	1.0	226	6	AW985398	NNV 134	C 465	20	1.0	445	9	CRI67302	CRI67302	Reverse s
C 393	20	1.0	228	6	C28342	Rice	C 466	20	1.0	448	2	BE860718	BE860718	UI-M-AL1-
C 394	20	1.0	243	1	AJ602547	AJ602547	C 467	20	1.0	449	6	CD730608	CD730608	4038937 1
C 395	20	1.0	246	2	BB376598	BB376598	C 468	20	1.0	449	6	CB742885	CB742885	ANGNNUC:N
C 396	20	1.0	249	2	BE127071	DEPA0820	C 469	20	1.0	453	6	CA021495	CA021495	H240E08
C 397	20	1.0	250	4	BU696352	BU696352	C 470	20	1.0	454	5	BO973693	BO973693	QH113001
C 398	20	1.0	256	6	CA715674	wk3c.pk0	C 471	20	1.0	457	6	CA693279	CA693279	wlm96.pk0
C 399	20	1.0	261	7	CF449068	EST685413	C 472	20	1.0	459	7	CN604794	CN604794	USDA.FP.1
C 400	20	1.0	272	2	BB404901	BB404901	C 473	20	1.0	462	1	AU070018	AU070018	AUT070018
C 401	20	1.0	272	5	BU882397	UM761E05	C 474	20	1.0	466	4	BG673922	BG673922	MINM53.WI
C 402	20	1.0	294	6	CD451406	USDA-PE.1	C 475	20	1.0	467	1	AU094366	AU094366	AU094366
C 403	20	1.0	296	8	BH229564	1006153A1	C 476	20	1.0	471	6	CF076930	CF076930	QHR14C05
C 404	20	1.0	303	6	CD711874	VVC025B05	C 477	20	1.0	471	1	AU082232	AU082232	AU082232
C 405	20	1.0	304	6	C28596	C28596	C 478	20	1.0	471	6	CB009693	CB009693	VVD004F08
C 406	20	1.0	309	2	BB164234	BB164234	C 479	20	1.0	471	6	CB911950	CB911950	VVD137H12
C 407	20	1.0	314	1	AV156120	AV156120	C 480	20	1.0	474	1	A1527911	A1527911	vj30E07.Y
C 408	20	1.0	324	6	CA358644	631400.NC	C 481	20	1.0	475	8	BH230076	BH230076	1006155H0
C 409	20	1.0	328	6	CA686747	wlm96.pk0	C 482	20	1.0	478	4	BG591632	BG591632	EST499474
C 410	20	1.0	331	6	CD711358	VVC025B05	C 483	20	1.0	483	5	BO995886	BO995886	OCG11E09
C 411	20	1.0	332	5	BY103114	BY103114	C 484	20	1.0	487	6	CD668301	CD668301	ecicL.pk0
C 412	20	1.0	333	6	CD191126	MS1-0068T	C 485	20	1.0	490	9	CG408876	CG408876	De570.Ds
C 413	20	1.0	335	1	AU069458	AU069458	C 486	20	1.0	492	1	AU395325	AU395325	AU395325
C 414	20	1.0	343	6	CB322164	EST0282.M	C 487	20	1.0	492	2	BE435261	BE435261	EST406339
C 415	20	1.0	344	2	AM269298	xs36d01.x	C 488	20	1.0	493	4	B1338401	B1338401	362166.MA
C 416	20	1.0	345	6	CA517485	KS09081C0	C 489	20	1.0	494	7	CN768392	CN768392	lat66E04
C 417	20	1.0	345	9	CR087542	Forward.s	C 490	20	1.0	497	7	CN744093	CN744093	SAL.US027
C 418	20	1.0	349	1	AU163327	AU163327	C 491	20	1.0	499	1	AU161382	AU161382	AU161382
C 419	20	1.0	353	2	AW326743	19681.MAR	C 492	20	1.0	503	2	BF642076	BF642076	NR031P051
C 420	20	1.0	353	6	CB914070	VVD008D10	C 493	20	1.0	508	1	A1992665	A1992665	701498357
C 421	20	1.0	355	1	AU069451	AU069451	C 494	20	1.0	508	4	BM136347	BM136347	WHR2608.G
C 422	20	1.0	358	2	BF321858	uz65d10.Y	C 495	20	1.0	510	2	AM751828	AM751828	QVI-CT011
C 423	20	1.0	363	8	BY035468	BY035468	C 496	20	1.0	510	4	B1797955	B1797955	H092P07.E
C 424	20	1.0	365	7	AZ134878	AZ134878	C 497	20	1.0	510	9	CE815919	CE815919	LI9T-GSS-
C 425	20	1.0	373	7	CO779500	CO779500	C 498	20	1.0	515	9	CG934620	CG934620	MBED107TR
C 426	20	1.0	374	6	CA029117	H264E01r	C 499	20	1.0	519	2	BE439917	BE439917	HTW1-532F
C 427	20	1.0	376	7	D41252	D41252	C 500	20	1.0	522	1	AL921277	AL921277	AL921277
C 428	20	1.0	378	5	BX835823	BX835823	C 501	20	1.0	522	6	CD883972	CD883972	FL.115A05
C 429	20	1.0	380	4	BG649500	EMI.80.B0	C 502	20	1.0	526	7	CF910684	CF910684	A0603C07
C 430	20	1.0	380	8	B1750890	B1750890	C 503	20	1.0	527	1	AU298769	AU298769	AU298769
C 431	20	1.0	380	8	BH229752	Ta01.02g1	C 504	20	1.0	527	6	CA655334	CA655334	wlm0.pk0
C 432	20	1.0	381	2	AM428824	Lj1tmpst	C 505	20	1.0	528	6	CB910568	CB910568	VVD152B04
C 433	20	1.0	381	2	BB844445	BB844445	C 506	20	1.0	529	6	CA661382	CA661382	wlmk1.pk0
C 434	20	1.0	382	1	AU069318	AU069318	C 507	20	1.0	531	6	CB718981	CB718981	AMGNNUC:C
C 435	20	1.0	383	5	BX836728	BX836728	C 508	20	1.0	531	6	CN904918	CN904918	010926ABD
C 436	20	1.0	385	5	BP095881	BP095881	C 509	20	1.0	534	5	BU868680	BU868680	M118H02.P
C 437	20	1.0	388	2	AM685205	NFC026F12N	C 510	20	1.0	534	6	CD475087	CD475087	na003-12m
C 438	20	1.0	389	1	AJ440591	AJ440591	C 511	20	1.0	536	4	BG909189	BG909189	Ta01.174H
C 439	20	1.0	392	2	BE116010	UI-R-B81-	C 512	20	1.0	537	7	CD581192	CD581192	BO201B02-
C 440	20	1.0	398	1	AU069368	AU069368	C 513	20	1.0	537	7	CF656134	CF656134	ta054E07
C 441	20	1.0	398	6	C97625	C97625	C 514	20	1.0	537	7	CK626526	CK626526	m23A08.Y
C 442	20	1.0	400	7	CO070313	GR.Fa27E	C 515	20	1.0	541	6	CD547847	CD547847	B0285C07
C 443	20	1.0	401	1	AV540214	AV540214	C 516	20	1.0	542	1	AU161185	AU161185	AU161185
C 444	20	1.0	402	4	BG096869	EST461388	C 517	20	1.0	542	7	CK934402	CK934402	CGF100425
C 445	20	1.0	402	6	CA002462	HS07J09r	C 518	20	1.0	543	5	BQ567640	BQ567640	g193h03.Y
C 446	20	1.0	404	7	D43598	D43598	C 519	20	1.0	544	1	A1896155	A1896155	EST265598
C 447	20	1.0	407	5	BO122054	EST607630	C 520	20	1.0	546	6	CB876723	CB876723	HP02D02T
C 448	20	1.0	409	6	CD213095	H91.28.G0	C 521	20	1.0	547	8	BM029055	BM029055	RP01-24-2
C 449	20	1.0	409	1	AU161252	AU161252	C 522	20	1.0	549	6	CB922232	CB922232	VVD081B08
C 450	20	1.0	409	5	BQ858881	E011887-0	C 523	20	1.0	549	6	CD474696	CD474696	na003-12m
C 451	20	1.0	412	2	BE847002	uw21e01.Y	C 524	20	1.0	550	9	BX523315	BX523315	BX523315
C 452	20	1.0	413	1	A1120709	ub72a06.r	C 525	20	1.0	553	6	CB322416	CB322416	HP-R-DY0-
C 453	20	1.0	419	2	BE946554	UI-M-BH3-	C 526	20	1.0	556	1	AA592307	AA592307	vo23A08.X
C 454	20	1.0	428	6	CA628059	w1e1.pk0	C 527	20	1.0	559	5	BU481945	BU481945	603847444
C 455	20	1.0	429	7	CA744746	w1e1c.pk0	C 528	20	1.0	559	5	CD887952	CD887952	G118.106K
C 456	20	1.0	429	7	CO541092	MdLrT3038	C 529	20	1.0	562	5	BU977465	BU977465	HAL1H16r
C 457	20	1.0	434	1	AL911110	AL911110	C 530	20	1.0	562	5	CB922795	CB922795	VVD088A12
C 458	20	1.0	434	6	CA692661	wlm96.pk0	C 531	20	1.0	562	6	B1863136	B1863136	tm6h07.Y
C 459	20	1.0	435	6	BH307919	CH230-4U1	C 532	20	1.0	568	4	CF912178	CF912178	A0627F09-
C 460	20	1.0	440	2	BE293896	601173044	C 533	20	1.0	569	7	BG907920	BG907920	Single re
C 461	20	1.0	441	2	BE192914	BE192914	C 534	20	1.0	571	3	CNS08EXU	CNS08EXU	
C 462	20	1.0	441	8	AQ816045	HS_5437_B	C 535	20	1.0	571	3			

C 536	20	1.0	571	6	CA654848	wlmo.pk00	609	20	1.0	658	7	CN847503	CN847503	EG07042B0
C 537	20	1.0	571	8	BZ249089	BZ249089 CH230-261	C 610	20	1.0	659	2	BE216915	BE216915	EST0458 T
C 538	20	1.0	575	5	CB008231	CB008231 VVCO5C06	611	20	1.0	660	8	AZ570798	AZ570798	278PvH01
C 539	20	1.0	578	4	BI473662	BI473662 fp40d12.Y	612	20	1.0	663	8	BZ512063	BZ512063	BOMR214TR
C 540	20	1.0	578	6	CA659125	CA659125 wlml.pk00	613	20	1.0	664	4	BI305444	BI305444	NLP_1.G18
C 541	20	1.0	578	6	CD890929	CD890929 G118.115M	614	20	1.0	664	6	CB916243	CB916243	VVD108D03
C 542	20	1.0	578	9	CG018800	CG018800 ZUADV46TV	615	20	1.0	665	1	AJ800922	AJ800922	AJ800922
C 543	20	1.0	579	5	BQ620385	BQ620385 TAlr1165F	616	20	1.0	667	6	CF211662	CF211662	CGF100066
C 544	20	1.0	579	6	CD817416	CD817416 BN20.041N	617	20	1.0	667	6	CB61303	CB61303	T22ATF TAM
C 545	20	1.0	581	6	C99251	C99251 C99251 R1ce	618	20	1.0	668	6	CD862783	CD862783	AZ01.104Y
C 546	20	1.0	581	7	CK767202	CK767202 wml01-7ms	619	20	1.0	669	6	CA817315	CA817315	CA12E1203
C 547	20	1.0	582	6	CA243486	CA243486 SCQGF1407	620	20	1.0	670	7	CF723779	CF723779	UI-M-GZ0-
C 548	20	1.0	585	7	CF449761	CF449761 EST686106	621	20	1.0	671	7	CO070312	CO070312	GR_Ea27E
C 549	20	1.0	585	9	FR0048387	FR0048387 Fugu rubr	622	20	1.0	672	2	AM133859	AM133859	fi1f107.Y
C 550	20	1.0	588	5	BQ240853	BQ240853 TaB05012B	623	20	1.0	673	2	BO410602	BO410602	GA_Ed003
C 551	20	1.0	588	4	BX087108	BX087108 BX087108	624	20	1.0	674	5	BO804242	BO804242	WHE5552 B
C 552	20	1.0	589	5	BI771687	BI771687 NF011A11F	625	20	1.0	675	4	BI921202	BI921202	EST541105
C 553	20	1.0	593	4	BI243821	BI243821 BI243821	626	20	1.0	675	6	CA342846	CA342846	672802 NC
C 554	20	1.0	593	6	CB812988	CB812988 VVD160C02	627	20	1.0	677	6	CF744209	CF744209	UI-M-GV0-
C 555	20	1.0	594	7	CE913024	CE913024 A0641H07-	628	20	1.0	677	6	CB005720	CB005720	VC025B05
C 556	20	1.0	594	7	CO783693	CO783693 BL018C GO	629	20	1.0	681	3	CNS0817Y	CNS0817Y	single re
C 557	20	1.0	599	5	BU045682	BU045682 PP_LBA002	630	20	1.0	682	6	CD890928	CD890928	115M
C 558	20	1.0	599	7	CF777360	CF777360 TaB05012B	631	20	1.0	686	5	BU039453	BU039453	PP_LBA000
C 559	20	1.0	606	5	BQ237794	BQ237794 TaB05012B	632	20	1.0	690	1	A1980300	A1980300	pat.pk002
C 560	20	1.0	607	1	AU094417	AU094417 AU094417	633	20	1.0	692	6	CD880613	CD880613	FI_075E21
C 561	20	1.0	607	6	CA676785	CA676785 wlm12.pk0	634	20	1.0	693	8	BH966736	BH966736	od127c11.
C 562	20	1.0	608	4	BM737493	BM737493 952056E05	635	20	1.0	694	9	AG301331	AG301331	Mus muscu
C 563	20	1.0	610	6	CD875341	CD875341 AZ03.104N	636	20	1.0	695	4	BM064115	BM064115	KS01063C0
C 564	20	1.0	610	7	CF656442	CF656442 TaB54e07.	637	20	1.0	695	7	CK949116	CK949116	4073966 B
C 565	20	1.0	612	4	BG573786	BG573786 602594877	638	20	1.0	696	4	BI955091	BI955091	HVSMW002
C 566	20	1.0	613	6	CA682253	CA682253 wlm124.pk0	639	20	1.0	698	7	CK263600	CK263600	EST709678
C 567	20	1.0	613	6	CB816586	CB816586 VVD111D05	640	20	1.0	705	5	BO996505	BO996505	OGG13A10.
C 568	20	1.0	614	8	BZ650280	BZ650280 OGCA277C	641	20	1.0	706	7	BX319785	BX319785	CA12E1203
C 569	20	1.0	617	6	CA070858	CA070858 SCUTAD103	642	20	1.0	706	8	BH423283	BH423283	BOMR214TR
C 570	20	1.0	618	6	CA269355	CA269355 SCBGR307	643	20	1.0	706	8	BH423283	BH423283	BOMR214TR
C 571	20	1.0	620	6	CA759582	CA759582 BR060005B	644	20	1.0	706	8	BH3938036	BH3938036	odf03E12.
C 572	20	1.0	620	6	CA759583	CA759583 BR060007B	645	20	1.0	707	6	CB340294	CB340294	CA23E102I
C 573	20	1.0	620	6	CB578941	CB578941 AMGNNUC:N	646	20	1.0	708	8	BE601936	BE601936	HVSMW010
C 574	20	1.0	621	5	BU994363	BU994363 HM06M12r	647	20	1.0	708	8	BZ375959	BZ375959	1e63e12.g
C 575	20	1.0	623	7	CF777103	CF777103 TaB09f08.	648	20	1.0	710	7	CF576349	CF576349	MCSA179A0
C 576	20	1.0	624	4	BM003510	BM003510 1031111A0	649	20	1.0	710	8	BH117090	BH117090	RPT-24.3
C 577	20	1.0	625	4	BM878778	BM878778 Pl6-C03 S	650	20	1.0	710	8	BH952227	BH952227	odh9a12.
C 578	20	1.0	625	9	CNS0401Z	CNS0401Z Tetraodon	651	20	1.0	712	2	BE858781	BE858781	Est#1PT7
C 579	20	1.0	630	9	CF413663	CF413663 CSECS027B	652	20	1.0	712	6	CF213190	CF213190	CGF100063
C 580	20	1.0	631	6	CD618039	CD618039 55114091J	653	20	1.0	713	3	CF232896	CF232896	CTA23X001
C 581	20	1.0	632	7	CN880366	CN880366 010417AAS	654	20	1.0	715	5	BO863251	BO863251	OGC33G04.
C 582	20	1.0	633	8	AO920598	AO920598 RPT-23-2	655	20	1.0	717	2	AM175049	AM175049	fi1f1E12.Y
C 583	20	1.0	634	5	BQ259329	BQ259329 fz97h09.Y	656	20	1.0	718	2	AM203151	AM203151	AM203151
C 584	20	1.0	636	6	CF213117	CF213117 CGF100063	657	20	1.0	722	7	CO536181	CO536181	ta112h05.
C 585	20	1.0	636	7	CN881117	CN881117 010425AAS	658	20	1.0	723	9	CG269706	CG269706	OGABT107C
C 586	20	1.0	638	5	BX645283	BX645283 DKFP781P	659	20	1.0	724	7	CK315956	CK315956	SB02028B1
C 587	20	1.0	639	5	CD873491	CD873491 AZ03.003H	660	20	1.0	724	8	BZ057547	BZ057547	1k9755a09.
C 588	20	1.0	640	6	CA569606	CA569606 wpa1c.pk0	661	20	1.0	725	6	CA815406	CA815406	CA12E1203
C 589	20	1.0	642	1	A1658024	A1658024 fc22d12.Y	662	20	1.0	725	6	CA817834	CA817834	CA12E1203
C 590	20	1.0	644	5	BQ998850	BQ998850 QG320G20.	663	20	1.0	728	7	CF800440	CF800440	M1M325 M
C 591	20	1.0	645	2	BE213667	BE213667 EST0357 T	664	20	1.0	731	9	CNS03MAJ	CNS03MAJ	AL505016
C 592	20	1.0	645	2	BE213674	BE213674 EST0365 T	665	20	1.0	733	1	AJ794246	AJ794246	TA794246
C 593	20	1.0	646	5	CD876127	CD876127 AZ03.108K	666	20	1.0	733	6	CA815916	CA815916	CA12E1301
C 594	20	1.0	646	6	CD874312	CD874312 AZ03.101N	667	20	1.0	737	7	CF219057	CF219057	DRNBXA09
C 595	20	1.0	646	6	CD894445	CD894445 G118.126E	668	20	1.0	739	6	CF233837	CF233837	Plac0026D
C 596	20	1.0	651	1	AU239156	AU239156 AU239156	669	20	1.0	742	9	CNS042BQ	CNS042BQ	AT771403
C 597	20	1.0	651	6	CD862014	CD862014 AZ01.102A	670	20	1.0	745	4	BS309101	BS309101	HVSMW000
C 598	20	1.0	651	6	CF211757	CF211757 CGF100066	671	20	1.0	746	4	BS672070	BS672070	DRNCBF02
C 599	20	1.0	652	7	CN943923	CN943923 010928AVB	672	20	1.0	754	4	BS671728	BS671728	DRNBXA09
C 600	20	1.0	652	6	CB914612	CB914612 VVD012H05	673	20	1.0	755	9	CC605217	CC605217	OGMBU11TH
C 601	20	1.0	653	4	BU567885	BU567885 BU567885	674	20	1.0	756	5	BU004395	BU004395	OGG5B11.Y
C 602	20	1.0	654	5	BE213532	BE213532 EST0222 T	675	20	1.0	756	9	CNS03WNE	CNS03WNE	TA639400
C 603	20	1.0	654	5	BX629100	BX629100 BX629100	676	20	1.0	760	7	CK215872	CK215872	FGAS02784
C 604	20	1.0	654	6	CB557548	CB557548 AMGNNUC:N	677	20	1.0	761	7	CK215684	CK215684	FGAS02765
C 605	20	1.0	654	7	CN941498	CN941498 010918AVB	678	20	1.0	761	9	BX996523	BX996523	Reverse s
C 606	20	1.0	657	8	AZ570929	AZ570929 280PvE03	679	20	1.0	763	6	CA368745	CA368745	645005 NC
C 607	20	1.0	658	8	CD876742	CD876742 AZ03.110M	680	20	1.0	765	5	BX861013	BX861013	BX861013
C 608	20	1.0	658	7	CP913260	CP913260 A0645H03-	681	20	1.0	770	9	CG327586	CG327586	OGMJB82TV

682	20	1.0	771	8	AQ869176	nbeb0034E	755	20	1.0	967	8	CC387004	CC387004	PURHP31TB
683	20	1.0	772	9	CC844186	NDL-8703.	756	20	1.0	967	9	CG396708	CG396708	ZMMB6C001
684	20	1.0	773	4	BG446500	GA-EB003	757	20	1.0	970	9	CG832404	CG832404	ZMMB0C012
685	20	1.0	774	4	BI733904	603355613	758	20	1.0	969	9	CL047856	CL047856	CH216-66P
686	20	1.0	774	7	CK772723	961295 MA	759	20	1.0	993	9	CNS04E4G	CNS04E4G	Tetraddon
687	20	1.0	775	5	BX869090	BX869090	760	20	1.0	993	9	CNS0364G	CNS0364G	Tetraddon
688	20	1.0	775	7	CN204870	Tor5256 G	761	20	1.0	1006	9	CNS020BQ	CNS020BQ	Tetraddon
689	20	1.0	777	7	CN203296	Tor3546 G	762	20	1.0	1009	9	CNS08EXV	CNS08EXV	Tetraddon
690	20	1.0	779	6	CB595784	AGENCOURT	763	20	1.0	1009	9	CNS03BRC	CNS03BRC	Tetraddon
691	20	1.0	783	6	CNS05JTB	AL246908	764	20	1.0	1010	9	CNS08RCR	CNS08RCR	Tetraddon
692	20	1.0	786	9	AG303553	Mus muscu	765	20	1.0	1028	9	CNS04LFO	CNS04LFO	Tetraddon
693	20	1.0	787	5	BX643868	DKFZp781P	766	20	1.0	1035	4	BM471782	BM471782	AGENCOURT
694	20	1.0	787	6	CD353587	UI-M-GM0-	767	20	1.0	1052	4	CNS08SW7	CNS08SW7	Single re
695	20	1.0	796	7	CK255367	EST739004	768	20	1.0	1054	3	CNS08SM6	CNS08SM6	Single re
696	20	1.0	798	7	CNS34460	UI-M-HS0-	769	20	1.0	1075	7	CK216031	CK216031	FGAS02800
697	20	1.0	798	9	CC457010	ZMMBBD014	770	20	1.0	1086	7	CK212435	CK212435	FGAS02430
698	20	1.0	801	7	CF448808	EST6985153	771	20	1.0	1104	7	CK212338	CK212338	FGAS02421
699	20	1.0	803	2	BF617530	HVSMBC001	772	20	1.0	1165	5	BQ481514	BQ481514	PV-GBA00
700	20	1.0	804	6	CA387503	669490 NC	773	20	1.0	1165	9	CL647240	CL647240	CH213-134
701	20	1.0	805	8	A2126212	OSJNB007	774	20	1.0	1199	7	CK211542	CK211542	FGAS02339
702	20	1.0	809	4	BM020213	603648802	775	20	1.0	1239	5	BQ433478	BQ433478	AGENCOURT
703	20	1.0	811	9	CC923999	L072114ba	776	20	1.0	1330	8	CC252781	CC252781	CH261-191
704	20	1.0	813	7	CNS29912	UI-M-HQ0-	777	20	1.0	1377	3	CR729663	CR729663	Tetraddon
705	20	1.0	813	9	CC972005	ZUHPD07TH	778	20	1.0	1381	2	BE917283	BE917283	Tetraddon
706	20	1.0	818	6	CB976208	CAE40001	779	20	1.0	1393	4	BG181131	BG181131	602329265
707	20	1.0	819	8	CK257469	EST741106	780	20	1.0	1439	3	CR730285	CR730285	Tetraddon
708	20	1.0	821	4	CG369396	HVSMB1002	781	20	1.0	1466	3	CR727014	CR727014	Tetraddon
709	20	1.0	821	6	BG369396	V-B-19G08	782	20	1.0	1558	2	BF343362	BF343362	602017521
710	20	1.0	821	6	CB288850	BONQD32TR	783	20	1.0	1579	2	CNS0A70T	CNS0A70T	Tetraddon
711	20	1.0	821	8	B2492400	603604977	784	20	1.0	1713	2	BF237925	BF237925	Arabidops
712	20	1.0	825	4	BI731966	603355828	785	20	1.0	2396	3	AK085066	AK085066	Mus muscu
713	20	1.0	826	6	CF210247	CAE20006	786	20	1.0	3061	3	AK045502	AK045502	Mus muscu
714	20	1.0	833	6	CB976623	CAE40002	787	20	1.0	3070	3	AK034476	AK034476	Mus muscu
715	20	1.0	833	6	CB976130	CAE40001	788	20	1.0	3681	3	AK082191	AK082191	Mus muscu
716	20	1.0	839	5	BU294050	603604977	789	20	1.0	129	4	BI430830	BI430830	949061F12
717	20	1.0	841	7	CK194594	FGAS00302	790	20	1.0	140	6	CB403622	CB403622	OSTR010C9
718	20	1.0	844	9	CG256899	OG0DU65TV	791	20	1.0	141	2	BE592936	BE592936	WS1-92-C0
719	20	1.0	850	8	B2190372	CH230-378	792	20	1.0	143	5	BU003721	BU003721	QGG36C16
720	20	1.0	851	6	CB976869	CAE40003	793	20	1.0	151	8	AZ592680	AZ592680	IMO403113
721	20	1.0	851	9	CL514687	SATL-892	794	20	1.0	185	5	BU005495	BU005495	QGG8R11.Y
722	20	1.0	858	7	CP616776	AGENCOURT	795	20	1.0	188	9	CE645918	CE645918	tiGr-g8S-
723	20	1.0	866	8	AZ558244	RPCT-23-2	796	20	1.0	198	9	CL624395	CL624395	OR-BB001
724	20	1.0	866	8	BH468052	BOHOU24TF	797	20	1.0	199	9	BH697244	BH697244	BOMB028TF
725	20	1.0	867	4	BG682141	602629436	798	20	1.0	200	8	BH146119	BH146119	BG01568-3
726	20	1.0	867	9	CG302905	OG0CC58TH	799	20	1.0	202	1	AV344438	AV344438	AV344438
727	20	1.0	870	5	BU557303	AGENCOURT	800	20	1.0	205	9	CNS07HAC	CNS07HAC	Anopheles
728	20	1.0	876	9	CNS026JC	AL183441	801	20	1.0	216	8	AZ072472	AZ072472	RPCT-23-4
729	20	1.0	882	4	BG196646	RST15872	802	20	1.0	218	7	D39814	D39814	RKCS1419A R
730	20	1.0	882	9	CC981689	ZDACY64TH	803	20	1.0	218	9	CR217060	CR217060	Reverse b
731	20	1.0	884	5	BQ715449	AGENCOURT	804	20	1.0	219	6	CB403255	CB403255	OSTR003H4
732	20	1.0	885	9	CNS01VOL	AL169374	805	20	1.0	225	5	BQ867189	BQ867189	QSD10A23
733	20	1.0	891	9	CG417256	ZMMB6C003	806	20	1.0	225	7	CN204931	CN204931	Tor53117 G
734	20	1.0	893	8	B2454381	BONKX80TR	807	20	1.0	227	9	CE607770	CE607770	tiGr-g8S-
735	20	1.0	894	9	CG089355	PUCVCV29TD	808	20	1.0	228	2	BM597730	BM597730	BBS97730
736	20	1.0	898	4	BI154955	602902760	809	20	1.0	232	1	AV113701	AV113701	AV113701
737	20	1.0	906	8	BZ755102	PUREF10TD	810	20	1.0	233	1	AJ770492	AJ770492	AJ770492
738	20	1.0	907	9	CC718705	OGUHU33TH	811	20	1.0	234	1	AA494656	AA494656	Fai10b1.X
739	20	1.0	911	9	CR201007	Forward s	812	20	1.0	236	7	D39872	D39872	RICS1516A R
740	20	1.0	921	9	CNS02ATK	AL188993	813	20	1.0	238	9	CE027689	CE027689	tiGr-g8S-
741	20	1.0	927	6	CB558023	AGENCOURT	814	20	1.0	239	8	AZ100984	AZ100984	RPCT-23-4
742	20	1.0	930	4	BG676499	602622860	815	20	1.0	240	1	AA824186	AA824186	VY20611.X
743	20	1.0	934	4	CK290232	EST752946	816	20	1.0	242	2	AA896507	AA896507	uY13907.X
744	20	1.0	936	4	BI948363	HVSMB1000	817	20	1.0	242	1	AA214731	AA214731	uY99B12.Y
745	20	1.0	938	2	BE214948	HV-CEB000	818	20	1.0	243	9	CR115916	CR115916	Reverse s
746	20	1.0	939	3	CNS08RCO	BX024870	819	20	1.0	249	9	CN873860	CN873860	001207AAR
747	20	1.0	943	9	CG327577	OGMUF82TH	820	20	1.0	251	5	BQ965597	BQ965597	QGG13R12
748	20	1.0	945	8	CC353901	POHEBD49TD	821	20	1.0	252	7	CO085307	CO085307	GR-EA02G
749	20	1.0	946	5	BU147813	AGENCOURT	822	20	1.0	258	6	CD060143	CD060143	MAT-0006P
750	20	1.0	953	8	BH156460	ENTFS63TR	823	20	1.0	264	6	CD450544	CD450544	USDA-FP-1
751	20	1.0	954	8	BZ755100	PUREF10TB	824	20	1.0	269	9	CL206131	CL206131	ZMMBBD057
752	20	1.0	955	2	BE418203	SCC022.FO	825	20	1.0	270	2	BE584984	BE584984	7-8C-20 P
753	20	1.0	961	9	CNS03QZS	Tetraddon	826	20	1.0	272	6	CA999795	CA999795	S234U-D10
754	20	1.0	965	3	CNS08L7Z	BX016923	827	20	1.0	272	1	AV113791	AV113791	AV113791

C 828	19	1.0	275	6	CA700199	CA7700199	WkMLC.pK0	C 901	19	1.0	339	6	CF327086	CF327086	NACL--01-
C 829	19	1.0	275	7	CK766222	CK766222	ltu01-13m	C 902	19	1.0	341	7	CF645659	CF645659	K39_A04_F
C 830	19	1.0	275	7	CN851191	CN851191	001001A1Af	C 903	19	1.0	341	7	D46796	D46796	RICS11694A
C 831	19	1.0	276	2	BN158036	BN158036	BL158036	C 904	19	1.0	341	9	CR037812	CR037812	Reverse s
C 832	19	1.0	276	9	CE466241	CE466241	tiGr-gss-	C 905	19	1.0	344	1	AV544699	AV544699	AV544699
C 833	19	1.0	278	8	BH171185	BH171185	SALK_0039	C 906	19	1.0	344	6	CB833114	CB833114	USDA-PP_1
C 834	19	1.0	280	1	AV080506	AV080506	AV080506	C 907	19	1.0	347	1	AV216352	AV216352	AV216352
C 835	19	1.0	282	1	AV156324	AV156324	AV156324	C 908	19	1.0	348	6	CF076877	CF076877	AMGNNUC.T
C 836	19	1.0	282	2	BE424168	BE424168	WHE0076_A	C 909	19	1.0	348	6	CG727954	CG727954	11190970D0
C 837	19	1.0	285	1	AJ772432	AJ772432	AJ772432	C 910	19	1.0	349	6	CF089765	CF089765	OHM23021
C 838	19	1.0	285	1	AJ772771	AJ772771	AJ772771	C 911	19	1.0	349	7	CN875476	CN875476	010204AAR
C 839	19	1.0	285	1	AV133589	AV133589	AV133589	C 912	19	1.0	349	7	CN851230	CN851230	001002AAR
C 840	19	1.0	286	1	AJ772364	AJ772364	BE054448	C 913	19	1.0	353	7	BO912459	BO912459	QHA20M13
C 841	19	1.0	286	2	BB054448	BB054448	BB054448	C 914	19	1.0	356	5	AZ794535	AZ794535	ZMO04HB22
C 842	19	1.0	286	8	BZ666396	BZ666396	SGT5680-3	C 915	19	1.0	360	8	AV736618	AV736618	AV736618
C 843	19	1.0	288	1	AV061868	AV061868	AV061868	C 916	19	1.0	361	1	BP345545	BP345545	602019116
C 844	19	1.0	288	6	CB213488	CB213488	OML03768	C 917	19	1.0	361	2	BP802363	BP802363	CMO-CT009
C 845	19	1.0	288	7	CF850710	CF850710	PSMA015XJ	C 918	19	1.0	361	2	CD490043	CD490043	TT31_H04_T
C 846	19	1.0	289	1	AV137010	AV137010	AV137010	C 919	19	1.0	361	6	CN656678	CN656678	rt-40a01.Y
C 847	19	1.0	289	1	AV522187	AV522187	AV522187	C 920	19	1.0	361	6	CD489215	CD489215	T20_C06_T
C 848	19	1.0	289	1	AV563133	AV563133	AV563133	C 921	19	1.0	362	6	CN860889	CN860889	000823AAF
C 849	19	1.0	291	5	BY390277	BY390277	BY390277	C 922	19	1.0	365	7	BY665030	BY665030	BY665030
C 850	19	1.0	292	1	AV010867	AV010867	AV010867	C 923	19	1.0	365	6	BI129871	BI129871	G096P70Y
C 851	19	1.0	293	4	BI038285	BI038285	RCS-NT026	C 924	19	1.0	367	4	AM706671	AM706671	SK01d05.Y
C 852	19	1.0	294	1	AT165324	AT165324	A08SP15u	C 925	19	1.0	368	2	CF091067	CF091067	QHM6P14.Y
C 853	19	1.0	295	1	AV145218	AV145218	AV145218	C 926	19	1.0	368	6	AM705601	AM705601	SK50B06.Y
C 854	19	1.0	295	2	BE444977	BE444977	WHE1130_G	C 927	19	1.0	369	2	CF644697	CF644697	K24_D03_F
C 855	19	1.0	295	4	BI15914	BI15914	sat65A014	C 928	19	1.0	369	8	BH229102	BH229102	1006150B0
C 856	19	1.0	295	8	AZ615809	AZ615809	OCG15D06	C 929	19	1.0	370	1	AT594531	AT594531	vc05F04.Y
C 857	19	1.0	297	5	BO860233	BO860233	OCG15D06	C 930	19	1.0	370	2	BF907354	BF907354	MRO-UT004
C 858	19	1.0	297	5	BT236117	BT236117	603408522	C 931	19	1.0	370	5	BY422279	BY422279	BY422279
C 859	19	1.0	300	1	AV008370	AV008370	AV008370	C 932	19	1.0	370	5	CA756828	CA756828	OC11D11_T
C 860	19	1.0	300	5	BU064720	BU064720	BU064720	C 933	19	1.0	372	6	AA024235	AA024235	ma01b12.Y
C 861	19	1.0	300	6	CS6252	CS6252	CS6252	C 934	19	1.0	373	4	BI319223	BI319223	949027D09
C 862	19	1.0	300	6	CS6970	CS6970	CS6970	C 935	19	1.0	374	4	CG827207	CG827207	ZMWB031
C 863	19	1.0	300	6	CS8261	CS8261	CS8261	C 936	19	1.0	374	7	T67258	T67258	yA53901.r4
C 864	19	1.0	300	7	D45986	D45986	RICS10319A	C 937	19	1.0	375	7	BU249018	BU249018	BU249018
C 865	19	1.0	302	9	CG645207	CG645207	OST389492	C 938	19	1.0	376	4	CE532315	CE532315	sav35D06
C 866	19	1.0	305	2	BE930748	BE930748	RC1-GN007	C 939	19	1.0	381	6	CA938619	CA938619	602070260
C 867	19	1.0	305	7	DA0833	DA0833	RICS2996A_R	C 940	19	1.0	381	6	BE526981	BE526981	602070260
C 868	19	1.0	305	8	AZ358393	AZ358393	1M0100L13	C 941	19	1.0	382	2	BE526981	BE526981	602070260
C 869	19	1.0	306	1	AA590789	AA590789	ym21c12.r	C 942	19	1.0	382	8	BM229147	BM229147	1006150D1
C 870	19	1.0	306	6	CL450875	CL450875	ZMWB047	C 943	19	1.0	383	1	AA615556	AA615556	vc09G03.T
C 871	19	1.0	308	6	CA004168	CA004168	HS16M13r	C 944	19	1.0	383	7	CK632397	CK632397	AM1-AP000
C 872	19	1.0	311	1	AA823689	AA823689	vm37901.r	C 945	19	1.0	384	2	BE426870	BE426870	QHE10P21_E
C 873	19	1.0	312	2	BE594222	BE594222	WS1_103_G	C 946	19	1.0	384	5	BU018681	BU018681	QHE10P21_E
C 874	19	1.0	313	1	AA981902	AA981902	ua34b11_r	C 947	19	1.0	384	8	BH229134	BH229134	1006150D0
C 875	19	1.0	313	7	CN849284	CN849284	000901A1F	C 948	19	1.0	385	2	BE661484	BE661484	402_GmAXS
C 876	19	1.0	314	8	BH916412	BH916412	3526_1_52	C 949	19	1.0	386	2	AM451554	AM451554	UT-H-BI3-
C 877	19	1.0	315	4	BJ086847	BJ086847	CF643297	C 950	19	1.0	386	2	BE376372	BE376372	601228751
C 878	19	1.0	315	7	CF643297	CF643297	D65_B03_F	C 951	19	1.0	386	6	CD490277	CD490277	T35_D05_T
C 879	19	1.0	316	5	BO869588	BO869588	OCGFB51TC	C 952	19	1.0	387	2	AM747173	AM747173	WS1_66_E0
C 880	19	1.0	316	8	BE723444	BE723444	OCGFB51TC	C 953	19	1.0	387	2	AM747173	AM747173	WS1_66_E0
C 881	19	1.0	317	6	CB857388	CB857388	DH0XG19ZB	C 954	19	1.0	387	5	BY394876	BY394876	BY394876
C 882	19	1.0	317	6	BI130639	BI130639	G108P61Y	C 955	19	1.0	387	6	FR0031119	FR0031119	Fuga_rubr
C 883	19	1.0	319	4	AV014053	AV014053	AV014053	C 956	19	1.0	387	7	BC241718	BC241718	RHT02_501
C 884	19	1.0	322	6	CA507600	CA507600	UI-R-FS1-	C 957	19	1.0	389	4	CN428776	CN428776	1700026001
C 885	19	1.0	322	6	CF327085	CF327085	NACL--01-	C 958	19	1.0	394	7	BX920294	BX920294	Reverse s
C 886	19	1.0	323	4	BG240392	BG240392	OVI_29_E0	C 959	19	1.0	394	9	CL260348	CL260348	01260348
C 887	19	1.0	324	8	AZ454883	AZ454883	1M0257G06	C 960	19	1.0	394	9	CG089121	CG089121	ut68C06.Y
C 888	19	1.0	325	5	BU493583	BU493583	NO_ADGR_D	C 961	19	1.0	395	4	BE089121	BE089121	ut68C06.Y
C 889	19	1.0	325	7	CF608112	CF608112	GEMMA01_0	C 962	19	1.0	395	8	AA693246	AA693246	vr58E09.s
C 890	19	1.0	326	1	AA608804	AA608804	af04e06_s	C 963	19	1.0	397	5	BO265893	BO265893	NISC_IF09
C 891	19	1.0	326	4	BO640361	BO640361	RST43051	C 964	19	1.0	397	8	AQ028925	AQ028925	CIT-HSP-2
C 892	19	1.0	326	5	BO667214	BO667214	OGD10C02	C 965	19	1.0	398	1	AT037401	AT037401	ub52C10.r
C 893	19	1.0	331	2	BE609955	BE609955	NXST_053_	C 966	19	1.0	398	6	CF293278	CF293278	30DGS--02
C 894	19	1.0	331	2	BE205987	BE205987	BB205987	C 967	19	1.0	398	7	CO788011	CO788011	NT003A_BI
C 895	19	1.0	331	2	CK099811	CK099811	A085P15_5	C 968	19	1.0	399	7	CA524576	CA524576	KS1204D00
C 896	19	1.0	332	6	CA640962	CA640962	wreln.pK0	C 969	19	1.0	400	6	CA933857	CA933857	MTU03T_P1
C 897	19	1.0	332	7	TS3901	TS3901	YB83e10_T1	C 970	19	1.0	400	6	CA933936	CA933936	MTU03T_P1
C 898	19	1.0	333	7	BF609643	BF609643	NXST_047	C 971	19	1.0	401	2	BF228417	BF228417	As_Lgz_27
C 899	19	1.0	333	7	CN861408	CN861408	001012AAG	C 972	19	1.0	402	8	AZ462586	AZ462586	1M0269L19
C 900	19	1.0	338	7				C 973	19	1.0	402	8			

ALIGNMENTS

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ORIGIN

Query Match 14.0%; Score 273; DB 8; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1627 CAGATTGGCGTGGTTGAGAAATGATCATCTGTCAGATCTTAAAGAAAGGATGAGA 1686
DB 169 CAGATTGGCGTGGTTGAGAAATGATCATCTGTCAGATCTTAAAGAAAGGATGAGA 228

QY 1687 CCAGGTCAAGCAGATGATATACGCTATACGAGGAGGACCGGATTTATGATCGAGCAG 1746
DB 229 CCAGGTCAAGCAGATGATATACGCTATACGAGGAGGACCGGATTTATGATCGAGCAG 288

QY 1747 TACATGAGAGCATGATGAGAAATGAGAAATGCGACCTTGGAATCAAGATACAGCC 1806
DB 289 TACATGAGAGCATGAGAAATGAGAAATGCGACCTTGGAATCAAGATACAGCC 348

QY 1807 ACGGGTGAATGAGTATCCGACGAGTACTGATGACCTGATCCGCTGTTCAAGCAGC 1866
DB 349 ACGGGTGAATGAGTATCCGACGAGTACTGATGACCTGATCCGCTGTTCAAGCAGC 408

QY 1867 GAGGGCCAAACCAACCGGAAATGAGATGGGG 1899
DB 409 GAGGGCCAAACCAACCGGAAATGAGATGGGG 441

RESULT 3
BZ455058 753 bp DNA linear GSS 13-DEC-2002
LOCUS BOKKA33TF.B0.1.6_2_KB.tot Brassica oleracea genomic clone BOKKA33,
DEFINITION BOKKA33TF.B0.1.6_2_KB.tot Brassica oleracea genomic clone BOKKA33,
ACCESSION BZ455058
VERSION BZ455058.1 GI:26731783
KEYWORDS GSS.

SOURCE
ORGANISM Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 753)
Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSS: BOKKA33TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.

FEATURES
source
1..753
Location/Qualifiers
/organism="Brassica oleracea"
/mol_type="Genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOKKA33"
/clone_1id="BO.1.6_2_KB.tot"
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total DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN

Query Match 9.6%; Score 187; DB 8; Length 753;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1282 AACACGATGTATCAACAGCTGTGATGGAACTTTGGGTACTTGCTCCGGAATACGCT 1341
DB 11 AACACGATGTATCAACAGCTGTGATGGAACTTTGGGTACTTGCTCCGGAATACGCT 70

QY 1342 GCAAGCGAAAAGCTCACGAGAAAGTCTGACGTTTCTCATTTGGCGTTGGTGGAG 1401
DB 71 GCAAGCGAAAAGCTCACGAGAAAGTCTGACGTTTCTCATTTGGCGTTGGTGGAG 130

QY 1402 CTCTATTCTGGAGGTGCACCCCGTTGATGCCAACATATCTATGATGACAGCTTAGT 1461
DB 131 CTCTATTCTGGAGGTGCACCCCGTTGATGCCAACATATCTATGATGACAGCTTAGT 190

QY 1462 GACTGGG 1468
DB 191 GACTGGG 197

RESULT 4
BX834233/c 853 bp mRNA linear EST 11-FEB-2004
LOCUS BX834233 Arabidopsis thaliana Adult vegetative tissue Col-0
DEFINITION BX834233 Arabidopsis thaliana cDNA clone G517L522ZF07 3PRIM, mRNA sequence.
ACCESSION BX834233
VERSION BX834233.1 GI:42517711
KEYWORDS EST.

SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 853)
Castelli,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpetelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL Unpublished (2004)
COMMENT Contact: Genome
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences).
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
http://www.genoscope.cns.fr/cgi-bin/gdb/gdb?source=Arabidopsis.

FEATURES
source
1..853
Location/Qualifiers
/organism="Arabidopsis thaliana"
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/clone="G517L522ZF07"
/tissue_type="Adult vegetative tissue"
/clone_1id="Arabidopsis thaliana Adult vegetative tissue
Col-0"

ORIGIN

Query Match 3.4%; Score 66; DB 5; Length 853;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 AACATGTCTATGTAGATGACAGCTTACTGATCGGACACACATTCCTTACCAGCA 1491
DB 668 AACATGTCTATGTAGATGACAGCTTACTGATCGGACACACATTCCTTACCAGCA 609

QY 1492 TCTGAG 1497
DB 11 TCTGAG 1497

Db 608 TCTGAG 603

RESULT 5
LOCUS CNS0440X

DEFINITION
CNS0440X 2106 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTSL71ZE12 of Adult vegetative tissue of strain col-0 of
Arabidopsis thaliana (thale cress).
BX823746

ACCESSION
VERSION BX823746.1 GI:42462388

KEYWORDS
HTC; GSLT cDNA.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
1 (bases 1 to 2106)
Castelli, V., Aury, J.M., Jallion, O., Mincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation

TITLE
Unpublished

JOURNAL
2 (bases 1 to 2106)

REFERENCE
Genoscope.

AUTHORS
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

JOURNAL
- Web : www.genoscope.cns.fr)

COMMENT
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallion O., Mincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers

FEATURES
source
1..2106
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSLTSL71ZE12"
/tissue_type="Adult vegetative tissue"
/plasmid="pCMVSPORT_6"
1..2106
/gene="At3g24550"

ORIGIN
gene

Query Match 3.4%; Score 66; DB 3; Length 2106;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 AACAAATCTATGTAGTACAGCTTATGTTACTGGGACGACCATGTTAAACCGAGCA 1491
DB 1520 AACAAATCTATGTAGTACAGCTTATGTTACTGGGACGACCATGTTAAACCGAGCA 1579

QY 1492 TCTGAG 1497
DB 1580 TCTGAG 1585

RESULT 6
LOCUS CD811645

314 bp mRNA linear EST 10-JUL-2003

DEFINITION
BN10.001E08F011207 BN10 Brassica napus cDNA clone BN10001E08, mRNA
sequence.
CD811645

ACCESSION
VERSION CD811645.1 GI:32493585

KEYWORDS
EST.

SOURCE
Brassica napus (rape)

ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
1 (bases 1 to 314)
Genoplane.
Genoplane, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplane

TITLE
JOURNAL

COMMENT
Genoplane

93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (http://www.genoplane.com
and http://genoplane-info.infobiogen.fr).

FEATURES
source
1..314
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jel Neuf"
/db_xref="taxon:3708"
/clone="BN10001E08"
/tissue_type="seed"
/clone_lib="BN10"

ORIGIN
Query Match 3.3%; Score 65; DB 6; Length 314;
Best Local Similarity 99.1%; Pred. No. 3.9e-22;
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1825 CCGACCAAGTACTATGACTGTACCCGTCGTGTTCAAGCAGCGGCAACACACGCG 1884
DB 1 CCGACCAAGTACTATGACTGTACCCGTCGTGTTCAAGCAGCGGCAACACACGCG 60

QY 1885 GAATGGAATGGGGAAGATTAAAGACACCGGTGAGGTTATAGTGAACCTTCTCT 1940
DB 61 GAGATGAGATGGGGAAGATTAAAGACACCGGTGAGGTTATAGTGAACCTTCTCT 116

RESULT 7
LOCUS CD811912

DEFINITION
CD811912 314 bp mRNA linear EST 10-JUL-2003
BN10.019G03F020121 BN10 Brassica napus cDNA clone BN10019G03, mRNA
sequence.

ACCESSION
VERSION CD811912

KEYWORDS
CD811912.1 GI:32493852

SOURCE
EST.

ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
1 (bases 1 to 314)
Genoplane.
Genoplane, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplane

TITLE
JOURNAL

COMMENT
Genoplane

93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (http://www.genoplane.com
and http://genoplane-info.infobiogen.fr).

FEATURES
source
1..314
Location/Qualifiers

			/organism="Brassica napus"
			/mol_type="mRNA"
			/cultivar="Uet Neuf"
			/db_xref="taxon:3708"
			/clone="BN10019G03"
			/tissue_type="seed"
			/clone_id="BN10"
ORIGIN			
Query Match	3.3%; Score 65; DB 6; Length 314;		
Best Local Similarity	99.1%; Pred. No. 3.9e-22;		
Matches 115; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
QY	1825 CCGACCACTGACTATGAGCTGTACCCTGGTTCAGTGCCGACGAGGCGCCAACCAACACGC	1884	
Db	1 CCGACCACTGACTATGAGCTGTACCCTGGTTCAGTGCCGACGAGGCGCCAACCAACACGC	60	
QY	1885 GAATGAGAGATGGGAAGATTAAAGAACCGCGTCAGAGGTATTAGTAGCCTTTCT	1940	
Db	61 GAGATGAGATGGGAAGATTAAAGAACCGCGTCAGAGGTATTAGTAGCCTTTCT	116	
RESULT 8			
AVS39333/c			
LOCUS	AVS39333 561 bp mRNA linear EST 20-FEB-2004		
DEFINITION	AVS39333 Arabidopsis thaliana roots Columbia Arabidopsis thaliana		
ACCESSION	CDNA clone R2130C07F 3, mRNA sequence.		
VERSION	AVS39333		
KEYWORDS	AVS39333.1 GI:8701090		
SOURCE	EST.		
ORGANISM	Arabidopsis thaliana (thale cress)		
	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
	1 (bases 1 to 561)		
REFERENCE	Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.		
AUTHORS	A large scale analysis of cDNA in Arabidopsis thaliana: Generation		
TITLE	of 12,028 non-redundant expressed sequence tags from normalized		
	size-selected cDNA libraries		
JOURNAL	DNA Res. 7 (3), 175-180 (2000)		
MEDLINE	20363093		
PUBMED	10907847		
COMMENT	Contact: Erika Asamizu		
	The First Laboratory for Plant Gene Research		
	Kazusa DNA Research Institute		
	Yana 1532-3, Kisarazu, Chiba 292-0812, Japan		
	Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.		
FEATURES			
Source	Location/Qualifiers		
	1..561		
	/organism="Arabidopsis thaliana"		
	/mol_type="mRNA"		
	/ecotype="Columbia"		
	/db_xref="taxon:3702"		
	/clone="R2130C07F"		
	/tissue_type="roots"		
	/clone_id="Arabidopsis thaliana roots Columbia"		
	/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:		
	XhoI"		
ORIGIN			
Query Match	2.7%; Score 53; DB 1; Length 561;		
Best Local Similarity	100.0%; Pred. No. 8.3e-16;		
Matches 53; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1579 GCTGCGGCTGTGTGCCCATTCAGCTGCGCGACAACCTCGCATAGCCAGAT	1631	
Db	543 GCTGCGGCTGTGTGCCCATTCAGCTGCGCGACAACCTCGCATAGCCAGAT	491	
RESULT 9			
AVS43493/c			
LOCUS	AVS43493 564 bp mRNA linear EST 20-FEB-2004		

DEFINITION	AY543493 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNA clone RZ2010f07 3', mRNA sequence.		
ACCESSION	AY543493		
VERSION	AY543493.1		
KEYWORDS	GI:8714907		
SOURCE	EST.		
ORGANISM	Arabidopsis thaliana (thale cress)		
REFERENCE	Arabidopsis thaliana		
AUTHORS	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 584)		
TITLE	Asamizu,E., Nakamura,Y., Sato,S. and Tabeta,S.		
	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries		
JOURNAL	DNA Res. 7 (3), 175-180 (2000)		
MEDLINE	20363093		
PUBMED	10907847		
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yena 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.		
FEATURES	Location/Qualifiers		
SOURCE	1..584		
	/organism="Arabidopsis thaliana"		
	/mol_type="mRNA"		
	/ecotype="Columbia"		
	/db_xref="taxon:3702"		
	/clone="RZ2010f07P"		
	/tissue_type="roots"		
	/clone_id="Arabidopsis thaliana roots Columbia"		
	/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"		
ORIGIN			
Query Match	2.7%;	Score 53;	DB 1; Length 584;
Best Local Similarity	100.0%;	Pred. No. 8.3e-16;	
Matches	53;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Cy	1579	GCTGGCGGCTTGTTGTCGCATTACGCTGCGCGAGACCTGCGATGAGCCAGAT	1631
Db	468	GCTGGCGGCTTGTTGTCGCATTACGCTGCGCGAGACCTGCGATGAGCCAGAT	416
RESULT 10			
LOCUS	BH432371 754 bp DNA linear GSS 12-DEC-2001		
DEFINITION	BOGVQ93TR BOGV Brassica oleracea genomic clone BOGV93, genomic survey sequence.		
ACCESSION	BH432371		
VERSION	BH432371		
KEYWORDS	GSS.		
SOURCE	GSS.		
ORGANISM	Brassica oleracea		
	Brassica oleracea		
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 754)		
REFERENCE	Town,C.D., Van Aken,S., Utechtack,T., Koo,H. and Fraser,C.M.		
AUTHORS	Whole genome shotgun sequencing of Brassica oleracea		
TITLE	Unpublished (2001)		
JOURNAL	Other GSSs: BOGVQ93TF		
COMMENT	Contact: Chris Town		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA.		
	Tel: 301-838-3523		
	Fax: 301-838-0208		
	Email: cdtown@tigr.org		
	DNA is from a doubled haploid provided by Tom Osborn.		
	Seq primer: TR		
	Class: sheared ends.		
FEATURES	Location/Qualifiers		

source 1. .754
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOGV93"
 /note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 2.28; Score 42; DB 8; Length 754;
 Best Local Similarity 100.0%; Pred. No. 5.2e-10;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1762 AAGAGTTTGAAGAAATGGACCTTGGAACTCAAGATACAC 1803
 Db 462 AAGAGTTTGAAGAAATGGACCTTGGAACTCAAGATACAC 503

RESULT 11
 BZ456327 342 bp DNA linear GSS 13-DEC-2002
 LOCUS BONEB66TR_BO_1.6_2_KB_tot Brassica oleracea genomic clone BONEB66,
 DEFINITION genomic survey sequence.
 ACCESSION BZ456327
 VERSION BZ456327.1 GI:26734454
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 342)
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
 REFERENCE Whole genome shotgun sequencing of Brassica oleracea
 TITLE Unpublished (2001)
 JOURNAL
 COMMENT Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.
 FEATURES
 source location/Qualifiers
 1. .342
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BONEB66"
 /clone_1lb="BO_1.6_2_KB_tot"
 /note="Vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 1.68; Score 32; DB 8; Length 342;
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 CCATCTCCACCATCAACTCCACACACACAC 68
 Db 182 CCATCTCCACCATCAACTCCACACACACAC 213

RESULT 12
 BZ066106 744 bp DNA linear GSS 10-OCT-2002
 LOCUS BZ066106/c
 DEFINITION 1j170e12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
 sequence.
 ACCESSION BZ066106

VERSION BZ066106.1 GI:23679353
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 744)
 REFERENCE Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.
 TITLE Whole genome shotgun reads from Brassica oleracea
 JOURNAL Unpublished (2002)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.edu
 Plate: 1j170 row: e column: 12
 Seq primer: -28RPOT reverse
 Class: shotgun
 High quality sequence start: 17
 High quality sequence stop: 551.
 FEATURES
 source location/Qualifiers
 1. .744
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_1lb="B.oleracea002"
 /note="Vector: POTW13; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear
 prep using Brassica oleracea T01000DH3 buds provided by
 Thomas Osborn at the University of Wisconsin. Genomic
 DNA was provided by Pablo Rabinowicz (CSHL) and the
 shotgun library prepared at Washington University Genome
 Sequencing Center."

ORIGIN

Query Match 1.58; Score 30; DB 8; Length 744;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 CCATTGAGCTCGCCGAGACCTCGCATGAG 1625
 Db 729 CCATTGAGCTCGCCGAGACCTCGCATGAG 700

RESULT 13
 C1469889/c 925 bp DNA linear GSS 01-APR-2004
 LOCUS SAIL_135_B06.v1 SAIL Collection Arabidopsis thaliana genomic clone
 DEFINITION SAIL_135_B06.v1, genomic survey sequence.
 ACCESSION C1469889
 VERSION C1469889.1 GI:45935600
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 925)
 REFERENCE Sessions,A., Burke,E., Presting,G., Aux,G., McEliver,J., Paton,D.,
 Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,D., Cotton,D.,
 Bullis,D., Snell,D., Miguel,T., Hutchinson,D., Kimerly,B.,
 Mitxel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
 TITLE A high-throughput Arabidopsis reverse genetics system
 JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
 MEDLINE 22356987
 PUBMED 12468722
 COMMENT Contact: Sessions A
 Applied Trait Genetics
 Syngenta Biotechnology Inc.
 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
 Email: allen.sessions@syngenta.com
 ABRC Stock Number CS806541; T-DNA left border flanking sequences of

Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.

FEATURES
source
Location/Qualifiers
1..925
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_135_B06_v1"
/note="SAIL Collection"
/note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"

ORIGIN

Query Match 1.5%; Score 30; DB 9; Length 925;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 CAGAGAGAGATGGCTCGCATGTGTGCTTG 1577
121 CAGAGAGAGATGGCTCGCATGTGTGCTTG 92

RESULT 14
LOCUS C0066237 472 bp mRNA linear EST 15-JUN-2004
DEFINITION Mafw2062306.y1 Mafw Mafus x domestica cDNA clone Mafw2062306.5'
similar to TR:Q9ZNO8 Q9ZNO8 PUTATIVE SERINE/THREONINE PROTEIN
KINASE.; mRNA sequence.
C0066237
C0066237.1 GI:48735718
EST.

ACCESSION C0066237
VERSION C0066237.1
KEYWORDS Mafus x domestica (cultivated apple)
SOURCE Mafus x domestica
ORGANISM Mafus x domestica

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Mafus.
1 (bases 1 to 472)
Korban, S., Vokhn, L., Liu, L., Gasic, K., Gonzales, O., Hernandez, A., Aldwinckle, H., Malnoy, M., Carroll, N., Goldbrough, P., Orvis, K., Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Rutter, E., Ronko, I., Tesagarehivalli, R., Kennedy, S., Waterson, R., and Wilson, R.
Apple Functional Genomics grant - NSF 0321702
Unpublished (2004)

TITLE JOURNAL
COMMENT Contact: Schuyler S. Korban
Apple Functional Genomics grant - NSF 0321702
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Library materials provided by: Schuyler S. Korban Library
constructed by: A. Hernandez / K. Gasic Library sequenced by:
Washington University Genome Sequencing Center
Mafu EST name: aah50603.y1
Seq primer: -40UP from Gibco
High quality sequence stop: 472.
Location/Qualifiers
1..472

FEATURES
source
/organism="Mafus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="Mafw2062306"
/lab_host="DH10B ampicillin resistant"
/clone_lib="Mafw"
/note="Vector: DH10B ampicillin resistant; Site 1: NotI;
Site 2: EcoRI; Total RNA was extracted separately from
each stage (bud, balloon, open and after pollination).
using the 'pine tree' method. Poly(A)+mRNA was isolated

twice from total RNA from each stage using the Oligotex Direct mRNA kit (Qiagen). mRNA was reverse transcribed into double stranded cDNA using a modified oligo18(dT) primer with an identifying tag sequence (see table below). cDNAs from different stages were pooled in equal amounts before adaptor ligation. Tag identification when sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGGA; Stage 2 (balloon) insert 18(A)TCGGA; Stage 3 (open) insert 18(A)TCGCT; Stage 4 (after pollination) insert 18(A)TCGCT. Tag identification when sequencing from 3' end: Stage 1 (bud) TCCGAl8(T) insert; Stage 2 (balloon) TCCGAl8(T) insert; Stage 3 (open) ACCGAl8(T) insert; Stage 4 (after pollination) ACCGAl8(T) insert. Double stranded cDNAs were size selected (more than 450 bp), adaptor with EcoRI adapters at both ends and then digested with NotI. The cDNAs were then directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene). Identification of adaptors and tags in 5'-end sequenced clones: <vector>...TAAGCTT<End Vector><Start EcoRI adaptor>GATTCGAATTCGATGTGTGGG<End EcoRI adaptor><Start insert>...AAAAAAAAAAAAAAAA<End insert><Start Tag>TCGGA<End Tag><Start NotI site/Vector>GCGGCCGCCACCGCGG... The total number of white colony forming units (cfu) in the primary library before amplification was 1.1x10⁶ cfu (colony forming units). The background of empty clones was less than 1%. Inserts ranged from 0.5kb to 3 kb, as determined by PCR. Purified plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites flanking the cloned cDNA inserts. The purified PCR products, representing the entire cloned cDNA population, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10⁶ cfu. Background of empty clones was less than 1%

ORIGIN

Query Match 1.5%; Score 29; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 GAGATGGCTCGCATGTGTGCTGCTGC 1583
351 GAGATGGCTCGCATGTGTGCTGCTGC 379

RESULT 15
LOCUS BM061076 505 bp mRNA linear EST 11-SEP-2002
DEFINITION KS01026B11 KS01 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM061076
VERSION BM061076.1 GI:22781194
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Capsicum.
1 (bases 1 to 505)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G., and Choi, D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
Unpublished (2001)
Contact: Doll Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology

P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea

Tel: 82-42-860-4340

Fax: 82-42-860-4309

Email: doi@email.kr

High quality sequence stop: 505.

Location/Qualifiers

1. .505

/organism="Capsicum annuum"

/mol_type="mRNA"

/cultivar="Bukang"

/db_xref="taxon:4072"

/tissue_type="leaf inoculated with Xanthomonas campestris

pv. glycines"

/dev_stage="8 weeks after germination"

/clone_lib="KS01"

/note="Vector: pBluescript SK(-)"

ORIGIN

Query Match 1.5%; Score 29; DB 4; Length 505;

Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 TTGCTGATTTTGCTCTTGCTAAGATTGCT 1272

Db 58 TTGCTGATTTTGCTCTTGCTAAGATTGCT 86

Search completed: November 13, 2004, 15:31:16
Job time : 4240 secs